

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:24:47 ; Search time 30.2051 Seconds

(without alignments)
83.819 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 78
Sequence: 1 MDGSGXXXXGGPSSSEQI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

- 1: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1982.DAT:*
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- 9: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 13: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1995.DAT:*
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- 19: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1998.DAT:*
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- 22: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	69	88.5	20	AAV90737
2	69	88.5	70	AAV70817
3	69	88.5	70	AAV70821
4	69	88.5	78	AAV70819
5	69	88.5	78	AAV70823
6	69	88.5	16	AAV71407
7	69	88.5	192	AAV05434
8	69	88.5	20	AAW7805
9	69	88.5	192	AAW7808
10	69	88.5	192	AAW87808
				Mouse BAX amino acid
				Mouse neuroprotect
				Mouse neuroprotect
				Mouse BAX protein
				Mouse BAX protein
				Murine Bcl-2 assoc
				Murine Bcl-2 assoc
				Murine Bax poly pep
				Apoptotic regulator
				Rat BAX amino acid
				Human BAX amino acid
				Human neuroprotect
				Human neuroprotect
				Human truncated Bax
				Human truncated Bax
				Human Bax protein
				Human wild type Bax
				Human Bax protein
				A human Bcl-2 assco
				Human Bax protein
				Human Bax alpha pr
				Amino acid sequence
				Human Bax polypept
				Human bcl-2 associ
				Human bcl-2 associ
				Coding region of c
				Truncated Bax amin
				Aspergillus sojae
				Aspergillus oryzae
				Aspergillus oryzae
				Lactococcus lactis
				Novel human diagno
				Human immune/haema

ALIGNMENTS

RESULT	ID	AAV90737	standard; peptide; 20 AA.
XX	XX	AAV90737;	AC
XX	XX	17-AUG-2000 (first entry)	DT
XX	XX	Mouse BAX amino acid sequence 1 to 20 SEQ ID NO: 3.	DE
XX	XX	Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis; cell death; cancer; cytostatic.	KW
XX	XX	Mus musculus.	OS
XX	XX	WO200020446-A2.	PN
PD	PD	13-APR-2000.	
XX	XX	05-OCT-1999; 99WO-IB01680.	PF
PR	XX	05-OCT-1998; 98US-0166028.	
PA	XX	(UVMC-) UNIV MCGILL.	
PT	XX	Shore GC., Goping S;	
PT	XX	DR WPI; 2000-303740/26.	
PT	XX	BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer -	
PS	XX	Example 2; Page 53; 53pp; English.	

XX The present invention describes a pure protein (P1) comprising a BAX
 CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 CC apoptosis. The polypeptides and methods from the present invention are
 CC useful for identifying compounds which can then
 CC be used for treating cancer. The present sequence represents a mouse
 CC BAX peptide sequence of amino acids 1 to 20, which is used in an
 CC example from the present invention.

XX Sequence 20 AA:
 Query Match 88.5%; Score 69; DB 21; Length 20;
 Best Local Similarity 73.7%; Pred. No. 1e-05; 0; Mismatches 14;
 Matches 14; Conservative 0; Indels 5; Gaps 0; Gaps 0;

Qy 1 MDGSGXXXXGGPSSSEQI 19
 Db 1 MDGSGEQLGSGGPSSSEQI 19

RESULT 2
 AAY70817 standard; Protein; 70 AA.
 ID AAY70817;
 XX AAY70817;
 AC AAY70817;
 XX DT 31-JUL-2000 (first entry)
 XX DE Mouse neuroprotective truncated BAX protein, tBAX70.
 XX KW Mouse; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 XX OS Mus musculus.
 XX Key Location/Qualifiers
 Region 1..58
 FT /note= "N-terminal region of BAX alpha"
 Domain 59..70
 FT /label= "Partial BH3 domain
 FT /note= "BH3 domain in the full-length BAX alpha consists
 FT of amino acids 59-73"
 XX PN WO20023083-A1.
 XX PD 27-APR-2000.
 XX PR 22-OCT-1999; 99WO-US24747.
 XX PR 22-OCT-1998; 98US-0177315.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PT Johnson EM, Easton R;
 XX DR WPI; 2000-339513/29.
 XX PT truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 32; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein,
 CC TBX70 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 70 amino acids of mouse
 CC BAX alpha, that includes the N-terminal region and a portion of the BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,

RESULT 3
 AAY0821 standard; Protein; 70 AA.
 ID AAY0821;
 XX AAY0821;
 XX DT 31-JUL-2000 (first entry)
 XX DE Mouse neuroprotective truncated BAX protein tBAX70 mutant.
 XX KW Mouse; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 XX OS Mus musculus.
 XX Key Location/Qualifiers
 Region 1..58
 FT /note= "N-terminal region from BAX alpha"
 FT Domain 59..70
 FT /label= "Partial BH3 domain
 FT /note= "BH3 domain in the full-length BAX alpha consists
 FT of amino acids 59-73"
 FT Misc-difference 55
 FT /note= "Wild type Ser is substituted by Ala"
 FT Misc-difference 60
 FT /note= "Wild type Ser is substituted by Ala"
 XX PN WO20023083-A1.
 XX PD 27-APR-2000.
 XX PR 22-OCT-1999; 99WO-US24747.
 XX PR 22-OCT-1998; 98US-0177315.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PT Johnson EM, Easton R;
 XX DR WPI; 2000-339513/29.
 XX DR N-PDB; AAD00124.
 XX PT truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 34; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein,
 CC TBX70 mutant (tBAX70M), which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of BH3 domain from mouse BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,

CC spinal cord injury, head trauma and stroke.
 XX
 SQ Sequence 70 AA;

Query Match	88.5%	Score 69;	DB 21;	Length 70;
Best Local Similarity	73.7%	Pred. No.	4e-05;	
Matches	14;	Conservative	0;	Mismatches 5;
Db	1 MDGSGXXXXGGPTSSQI 19			

RESULT 4
 AAY70819
 ID AAY70819 standard; Protein: 78 AA.
 XX
 AC AAY70819;
 XX
 DT 31-JUL-2000 (first entry)
 DE Mouse neuroprotective truncated BAX protein, tBAX78.
 XX
 KW Mouse; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Region 1..58
 FT /note= "N-terminal region of BAX alpha"
 FT 59..73
 FT /label= BH3-domain
 XX
 PN WO200023083-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 22-OCT-1999; 99WO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PT Johnson EM, Easton R;
 XX
 DR WPI; 2000-319513/29.
 XX
 DR N-PSDB; AAD00126.
 XX
 PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 34-35; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of BH3 domain of mouse BAX alpha, and a novel
 CC C-terminal sequence of 8 amino acids not present in BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The BAX protein lacking only the
 CC domains of the full length BAX alpha. The BAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 Sequence 78 AA;

Query Match	88.5%	Score 69;	DB 21;	Length 78;
Best Local Similarity	73.7%	Pred. No.	4.5e-05;	
Matches	14;	Conservative	0;	Mismatches 5;
Db	1 MDGSGXXXXGGPTSSQI 19			

RESULT 6		RESULT 7	
AAR71407	ID	AAY05434	ID
AAR71407 standard; Protein; 192 AA..		AAY05434 standard; Peptide; 192 AA..	
XX	AC	XX	AC
XX	AAR71407;	XX	AAY05434;
XX	15-NOV-1995 (first entry)	XX	XX
XX	DE	DT	02-JUL-1999 (first entry)
DE	Murine Bax protein.	XX	
KW	Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.	KW	BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.
KW	OS	XX	OS
OS	Mus musculus.	XX	Mus sp.
PN	W09505750-A.	PN	W0916787-A1.
XX		XX	
PD	02-MAR-1995.	PD	08-APR-1999.
XX		XX	
PF	24-AUG-1994; 94WO-US09701.	PF	22-SEP-1998; 98WO-US19765.
XX		XX	
PR	26-AUG-1993; 93US-0112208.	PR	07-OCT-1997; 97US-0946039.
XX	25-MAY-1994; 94US-0248819.	PR	26-SEP-1997; 97US-0060133.
PA	(UNIW) UNIV WASHINGTON.	PA	(UNIW) UNIV WASHINGTON.
XX		XX	
PI	Korsmeyer SJ;	PT	Korsmeyer SJ;
XX		XX	
DR	WPI; 1995-106605/14.	DR	WPI; 1999-255058/21.
XX		XX	
PT	Methods for producing and identifying mutant bcl-2 proteins - that lack death repressor activity and/or lacks binding to Bax.	PT	Bcl homology domain 3 polypeptide
XX		XX	
PS	Disclosure; Fig 3; 133pp; English.	PS	Disclosure; Fig 21c; 104pp; English.
XX		XX	
CC	This sequence represents murine Bax protein. Bax is a protein which is associated with the bcl-2 alpha and beta proteins. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2 is a 26 kd membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T origins rather than directly promoting proliferation of these cell types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose response to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with this 21 kd protein, Bax. Overexpressed Bax accelerates apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death following an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion in the BH1 or BH2 domains. This makes the mutant protein substantially incapable of binding Bax and/or incapable of death repressor activity. Down regulation of bcl-2 is useful in cancer therapy, controlling hyperplasias and eliminating self-reactive clones in autoimmunity by favouring death effector molecules. Up regulating bcl-2 is beneficial in treatment and diagnosis of immuno-deficiency diseases, including AIDS and neurodegenerative and ischaemic cell death.	CC	This sequence represents the murine BAX protein. The invention relates to a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell, a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death regulation.
CC		CC	
CC	Sequence 192 AA;	Sequence 192 AA;	Sequence 192 AA;
CC	Query Match 88.5%; Score 69; DB 16; Length 192;	Query Match 88.5%; Score 69; DB 20; Length 192;	Query Match 88.5%; Score 69; DB 20; Length 192;
CC	Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;	Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;	Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;
CC			
CC	QY 1 MDGSGXXXXGGPSSSEQI 19	QY 1 MDGSGXXXXGGPSSSEQI 19	QY 1 MDGSGXXXXGGPSSSEQI 19
CC	Db 1 MDGSQEQLGGGGPSSSEQI 19	Db 1 MDGSQEQLGGGGPSSSEQI 19	Db 1 MDGSQEQLGGGGPSSSEQI 19
CC			
CC	RESULT 8	RESULT 8	RESULT 8
CC	AAW77805	AAW77805	AAW77805
XX	ID	ID	ID
XX	AAW87805 standard; Protein; 192 AA.	AAW87805 standard; Protein; 192 AA.	AAW87805 standard; Protein; 192 AA.
AC		AC	
AC	AAW87805;	AC	AAW87805;
XX		XX	
DT	10-MAR-1999 (first entry)	DT	10-MAR-1999 (first entry)
XX		XX	
DE	Murine Bcl-2 associated protein designated Bax.	DE	Murine Bcl-2 associated protein designated Bax.
XX		XX	
KW	Murine; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator; bcl-2-related function; apoptosis.	KW	Murine; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator; bcl-2-related function; apoptosis.
XX		XX	
SQ	Sequence 192 AA;	Sequence 192 AA;	Sequence 192 AA;
XX	Query Match 88.5%; Score 69; DB 16; Length 192;	Query Match 88.5%; Score 69; DB 20; Length 192;	Query Match 88.5%; Score 69; DB 20; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;	Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;	Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 14; Mismatches 5; Indels 0; Gaps 0;	
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY 1 MDGSGXXXXGGPSSSEQI 19	OY 1 MDGSGXXXXGGPSSSEQI 19	OY 1 MDGSGXXXXGGPSSSEQI 19	
Db 1 MDGSQEQLGGGGPSSSEQI 19	Db 1 MDGSQEQLGGGGPSSSEQI 19	Db 1 MDGSQEQLGGGGPSSSEQI 19	

OS	MUS	SP.
XX	US5856171-A.	
PN		
PD	05-JAN-1999.	
XX		
PF	10-NOV-1994;	94US-0337646.
PR	10-NOV-1994;	94US-0337646.
PR	26-AUG-1993;	93US 011208.
PR	25-MAY-1994;	94US-0248819.
XX		
PA	(UNIW) UNIV WASHINGTON.	
XX		
PI	Korsmeyer SJ;	
XX		
DR	WPI; 1999-105119/09.	
XX		
PT	DNA composition encoding bcl-2 two-hybrid and reporter system - for identifying modulators of bcl-2 function	
XX		
PS	Example 10: Fig 7; 10pp; English.	
XX		
CC	The present sequence represents a murine Bcl-2 associated protein designated Bax. The Bax protein is used in a composition which comprises a bcl-2 family member polypeptide, a naturally occurring Bax polypeptide and an antibody, that binds to the Bax polypeptide. The composition is used to identify modulators of bcl-2-related function, e.g. substances that inhibit binding of Bax to bcl-2, which would be potentially useful as drugs for modulating apoptosis.	
CC		
SQ	Sequence 192 AA;	
Query Match	88.5%; Score 69; DB 20; Length 192;	
Best Local Similarity	73.7%; Pred. No. 0.00012;	
Matches	14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY	1 MDGSGXXXGGPTSSQI 19	
OY		
Db	1 MDGSGQLGSGCPTSSQI 19	
XX		
AC	AAY70828;	
XX		
DT	31-JUL-2000 (first entry)	
XX		
DE	mouse BAX alpha protein.	
XX		
KW	mouse; truncated BAX protein; TBAX; BAX alpha; BCL-2 family; head trauma; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.	
XX		
OS	Mus musculus.	
XX		
RESULT	9	
AAW87808		
ID	AAW87808 standard; Protein; 192 AA.	
XX		
AC	AAW87808;	
XX		
DT	10-MAR-1999 (first entry)	
XX		
DE	Murine Bcl-2 associated protein designated Bax.	
XX		
KW	Bcl-2 associated protein; Bax; bcl-2; antibody; modulator; bcl-2-related function; apoptosis.	
XX		
OS	Mus sp.	
XX		
PN	US5856171-A.	
PD	05-JAN-1999.	
XX		
PF	10-NOV-1994;	94US-0337646.
PR	10-NOV-1994;	94US-0337646.
PR	26-AUG-1993;	93US 011208.
PR	25-MAY-1994;	94US-0248819.
XX		
PA	(UNIW) UNIV WASHINGTON.	
XX		
PI	Korsmeyer SJ;	
XX		
DR	WPI; 1999-105119/09.	
XX		
PT	Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -	
XX		

PS	Disclosure:	Page 36-37; 43pp; English.
CC	The present sequence is a mouse BAX alpha protein, a pro-apoptotic protein which is a member of BCL-2 family of proteins that are involved in regulation of neuronal programmed cell death. The patent discloses specific truncated proteins derived from BAX alpha which inhibit neuronal apoptosis induced by trophic factor deprivation. The anti-apoptotic truncated BAX (tBAX) proteins include tBAX70, tBAX18 and their mutants. These proteins contain the N-terminal region and at least a portion of the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal transmembrane domains. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The tBAX proteins are used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.	CC
CC	CC	CC
XX	Sequence	192 AA;
XX	Query Match	88 %;
XX	Best Local Similarity	73.7%;
XX	Matches	14;
XX	DB	21;
XX	Score	69;
XX	Pred.	No. 0.00012;
XX	Mismatches	0;
XX	Indels	5;
XX	Gaps	0;
XX	RESULT 11	
ID	AAB74122	
ID	AAB74122 standard; Protein; 192 AA.	
AC	AAB74122;	
XX		
PT	22-MAY-2001	(first entry)
DE	Murine bcl-2 associated x protein (Bax) #1.	
XX		
KW	Murine; Bax; cytostatic; immunosuppressive; immunostimulant; infection; apoptosis modulator; bcl-2 associated x protein; cancer therapy; AIDS; autoimmunity; immunodeficiency; reperfusion injury; stroke; aging; myocardial infarction; traumatic brain injury; ischaemia; neurodegenerative diseases; hepatitis; transplant rejection; toxemia; lymphoproliferative disease.	
KW		
OS	Mus sp.	
XX		
PN	US6184202-B1.	
XX		
PD	06-FEB-2001.	
XX		
PF	11-SEP-1997;	97US-0927326.
XX		
PR	10-NOV-1994;	94US-0337646.
PR	26-AUG-1993;	93US-0112208.
PR	25-MAY-1994;	94US-024819.
XX		
PA	(UNIW) UNIV WASHINGTON.	
XX		
PI	Korsmeyer SJ;	
XX		
DR	WPI; 2001-256104/26.	
XX		
PT	Modulating apoptosis of a cell, useful in maintaining homeostasis in adult tissues, or treating proliferative or autoimmune diseases, comprising administering a BHL domain or BH2 domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL bcl-2 associated x protein	
XX		
PS	Example 6; Fig 3; 105pp; English.	

CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially useful in cancer therapy and treating autoimmunity, immunodeficiency diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke, traumatic brain injury, neurodegenerative diseases, aging, ischaemia, toxemia, infection, hepatitis, transplant rejection, and lymphoproliferative diseases. The present sequence is murine Bax, which was used in the method of the present invention.

KW cell death; cancer; cytostatic.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Rattus norvegicus.
 XX
 FH Location/Qualifiers
 FT Misc-difference 6 /label= Glu, Asp
 FT Misc-difference 7 /label= Gln, His
 FT Misc-difference 8 /label= Leu, Pro
 FT Misc-difference 9 /label= Arg, Gly
 FT Misc-difference 10 /label= Ser, Gly
 XX
 PN WO2000020446-A2.
 XX
 PD 13-APR-2000.
 XX
 PR 05-OCT-1999; 99WO-1B01680.
 XX
 PR 05-OCT-1998; 98US-0166028.
 PA (UVMC - UNIV MCGILL.
 XX
 PI Shore DC, Goping S;
 XX
 DR WPI: 2000-303740/26.
 XX
 PT BAX polypeptide lacking an ART domain, useful for identifying agents
 PT that modulate apoptosis which can then be used for treating cancer -
 PS disclosure; Page 6; 53pp; English.

XX
 CC The present invention describes a pure protein (P1) comprising a BAX
 CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 CC apoptosis. The polypeptides and methods from the present invention are
 CC useful for identifying compounds that modulate apoptosis which can then
 CC be used for treating cancer. The present sequence represents a consensus
 CC sequence for an ART domain derived from human, mouse and rat, which is
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 19 AA;

Query Matchⁿ 87.2%; Score 68; DB 21; Length 19;

Best local Similarity 100.0%; Pred. No. 1.5e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0;

Qy 1 MDSGXXXXGGTSSEQI 19
 Db 1 ||||||| 19
 1 MDSGXXXXGGTSSEQI 19

GeNCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:36:33 ; Search time 24.359 seconds
(w/out alignments)
160.717 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 19
Sequence: 1 MDGSGXXXXGGPSSQI 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 20604715 residues
Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTRMBL_21:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_oranelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_rodent:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_tvirus:*
- 16: sp_bacteriapl:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	9	47.4	24	4 Q8WXL1	Q8WXL1 PRELIMINARY; PRT; 24 AA.
2	9	47.4	24	11 Q8VHY7	Q8VHY7 ID: Q8VHY1; PRELIMINARY; PRT; 24 AA.
3	9	47.4	164	4 Q9uqd6	Q9uqd6 Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
4	9	47.4	179	4 Q8WYg7	Q8WYg7 homologous protein best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
5	6	31.6	45	4 Q9h039	Q9h039 homologous protein best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
6	6	31.6	192	6 Q8sq43	Q8sq43 felis silvestris best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
7	6	31.6	297	4 Q8WV5	Q8WV5 homologous protein best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
8	6	31.6	297	13 Q98107	Q98107 xenopus laevis best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
9	6	31.6	312	4 Q98V93	Q98V93 homologous protein best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
10	6	31.6	313	12 Q8B450	Q8B450 sigma virus best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
11	6	31.6	315	17 Q8tIC5	Q8tIC5 metchnikovia best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
12	6	31.6	364	6 Q28129	Q28129 bos taurus best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
13	6	31.6	411	10 Q9SH58	Q9SH58 arabidopsis best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
14	6	31.6	447	5 Q17816	Q17816 caenorhabditis best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
15	6	31.6	604	15 Q8q880	Q8q880 human immunodeficiency virus best local similarity 100.0% (TREMBLrel. 20, Last sequence update)
16	5	31.6	625	5 Q9NE37	Q9NE37 leishmania best local similarity 100.0% (TREMBLrel. 20, Last sequence update)

ALIGNMENTS

RESULT 1

ID	SEQUENCE	DESCRIPTION
Q8WXL1	Q8WXL1	PRELIMINARY; PRT; 24 AA.
Q8VHY1	Q8VHY7	PRELIMINARY; PRT; 24 AA.
Q9uqd6	Q9uqd6	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q8WYg7	Q8WYg7	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q9h039	Q9h039	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q8sq43	Q8sq43	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Felis silvestris
Q8WV5	Q8WV5	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Xenopus laevis
Q98107	Q98107	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Xenopus laevis
Q98V93	Q98V93	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q8B450	Q8B450	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Sigma virus
Q8tIC5	Q8tIC5	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Metchnikovia
Q28129	Q28129	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Bos taurus
Q9SH58	Q9SH58	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Arabidopsis thaliana
Q17816	Q17816	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Caenorhabditis elegans
Q8q880	Q8q880	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Human immunodeficiency virus
Q9NE37	Q9NE37	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Leishmania

RESULT 2

ID	SEQUENCE	DESCRIPTION
Q8VHY7	Q8VHY7	PRELIMINARY; PRT; 24 AA.
Q8WYg7	Q8WYg7	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q9h039	Q9h039	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q8sq43	Q8sq43	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Felis silvestris
Q8WV5	Q8WV5	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Xenopus laevis
Q98107	Q98107	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Xenopus laevis
Q98V93	Q98V93	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Oryzsa sativa
Q8B450	Q8B450	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Sigma virus
Q8tIC5	Q8tIC5	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Metchnikovia
Q28129	Q28129	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Bos taurus
Q9SH58	Q9SH58	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Arabidopsis thaliana
Q17816	Q17816	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Caenorhabditis elegans
Q8q880	Q8q880	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Human immunodeficiency virus
Q9NE37	Q9NE37	Best Local Similarity 100.0%; Score 9; DB 4; Length 24; Matches 9; Conservativeness 0; Pred. No. 0; 0 0 0 0; Mismatches 0; Indels 0; Gaps 0; Leishmania

DE Bcl2-associated X protein (Fragment).
 GN BAX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=1090;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=BALB/C;
 RA Thorborow E.C., Schwartzfarb F.M., Manfredi J.J.;
 RT "A conserved intronic response element mediates direct p53-dependent
 transcriptional activation of both the human and murine bax genes.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR33905; ALA7334.1; -;
 NON_TER 24 24 MW;
 SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

Query Match 47.4%; Score 9; DB 11; Length 24;
 Best local Similarity 100.0%; Pred. No. 0.0056; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
 Db 11 GGPTSSEQI 19

RESULT 3

Q9HQD6	PRELIMINARY;	PRT; 164 AA.
ID	Q9HQD6	
AC	Q9HQD6;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Bax epsilon.	
OS	Homo sapiens (Human).	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RC	NCBI_TAXID=9606;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN;	
RX	MEDLINE=99120940; PubMed=9920818;	
RA	Shi, B.; Tribe D.; Kajiji S.; Iwata K.K.; Bruskin A.; Mahajna J.;	
RT	"Identification and characterization of baxepsilon, a novel bax variant missing the BH2 and the transmembrane domains.";	
RL	Biochem. Biophys. Res. Commun. 254:779-785(1999).	
DR	EMBL; AB00786; ADP2205.1; -;	
DR	InterPro; IPR00712; BCL2_BH.	
DR	InterPro; IPR02415; BCL2_family.	
DR	Pfam; PF00452; BCL2_2; 1.	
DR	SMART; SM00337; BCL2; 1.	
DR	PROSITE; PS50062; BCL2_FAMILY; 1.	
DR	PROSITE; PS01080; BHL; 1.	
DR	PROSITE; PS01259; BH3; 1.	
DR	SEQUENCE 164 AA; 18129 MW; 12CCDBB073EF4C9E CRC64;	
QY	47.4%; Score 9; DB 4; Length 164;	
QY	Best Local Similarity 100.0%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;	
QY	11 GGPTSSEQI 19 Db 11 GGPTSSEQI 19	

RESULT 4

Q9NYG7	PRELIMINARY;	PRT; 179 AA.
ID	Q9NYG7	
AC	Q9NYG7;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Bax-signal.	

Query Match 47.4%; Score 9; DB 4; Length 164;
 Best Local Similarity 100.0%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
 Db 11 GGPTSSEQI 19

RESULT 5

Q9HQ39	PRELIMINARY;	PRT; 45 AA.
ID	Q9HQ39	
AC	Q9HQ39;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE	Hypothetical 5.1 kDa protein (Fragment).	
GN	DKFP547M14.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RC	NCBI_TAXID=9606;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN;	
RA	Blocker H.; Boecher M.; Brandt P.; Meves H.W.; Weil B.; Wiemann S.;	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AL512745; CAD21671.1; -;	
KW	Hypothetical protein.	
FT	NON_TER 1 1	
SQ	SEQUENCE 45 AA; 5069 MW; 64557BA7DB929BB7 CRC64;	

Query Match 31.6%; Score 6; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;

QY 14 TSSDOI 19
 Db 14 TSSDOI 19

RESULT 6

Q8S243	PRELIMINARY;	PRT; 192 AA.
ID	Q8S243	
AC	Q8S243;	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Bax-protein.	
GN	BAX.	
OS	Felis silvestris catus (Cat).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1] SPQUENCE FROM N.A.
RA Yamazaki J., Oguna K., Kano R., Hasegawa A.;
RT "molecular cloning of feline bcl-2 family.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB080724; BAB85810.1; -;
SEQUENCE 192 AA; 21283 MW; 852D271AE86923FB CRC64;
SQ

Query Match 31.6%; Score 6; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TSSEQL 19
Db 14 TSSEQL 19

RESULT 7
O9BVV5 PRELIMINARY; PRT; 297 AA.
ID O9BVV5:
AC O9BVV5:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Hypothetical 33.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea;
OC NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=PLACENTA;
RC Strauberg R.;
DR Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR001012; UBX.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00789; UBX; 1.
DR SMART: SM00165; UBA; 1.
DR SMART; SM00166; UBX; 1.
DR HYPOTHEtical protein.
SQ SEQUENCE 297 AA; 33325 MW; E4E0C8BBAC93F2BB CRC64;

Query Match 31.6%; Score 6; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 71; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSEQ 18
Db 64 PTSSEQ 69

RESULT 8
008107 PRELIMINARY; PRT; 297 AA.
ID 008107:
AC 008107:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (Fragment).
GN IRBP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodidae; Xenopus.
RN [1] NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=93366942; PubMed=8360278;

RESULT 9
O9BV93 PRELIMINARY; PRT; 312 AA.
ID O9BV93:
AC O9BV93:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Similar to O9BV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea;
OC NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=COLON;
RC Strauberg R.;
DR Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: BC00132; AAH0132.1; -
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR001012; UBX.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00789; UBX; 1.
DR SMART: SM00165; UBA; 1.
DR SMART; SM00166; UBX; 1.
DR SMART; SM00166; UBX; 1.
DR SMART; SM00166; UBX; 1.
SQ SEQUENCE 312 AA; 35107 MW; 75C94CB67C03EB78 CRC64;

Query Match 31.6%; Score 6; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 74; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSEQ 18
Db 64 PTSSEQ 69

RESULT 10
088450 PRELIMINARY; PRT; 313 AA.
ID 088450:
AC 088450:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 14, Last annotation update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nonstructural DE phosphoprotein).
DE P.
OS Sigma virus.
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TextID=11301;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96074506; PubMed=7491755;
 RA Landes-Bervaud C., Bras F., Dezelee S., Tenings D.;
 RT "Gene 2 of the sigma rhabdovirus genome encodes the P protein, and
 gene 3 encodes a protein related to the reverse transcriptase of
 retroviruses";
 RL Virology 213:300-312(1995).
 DR EMBL; X6102; CAK62514.1; -.
 DR FlyBase; FBgn0015610; Sigma Virus\p.
 KW Transferase; RNA-directed RNA polymerase; Phosphorylation;
 SQ Nonstructural protein; Sequence 313 AA; 35247 MW; 8G5484FED2038E3F CRC64;

Query Match 31.6%; Score 6; DB 12; Length 313;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PTSEQ 18
 Db 222 PTSEQ 227

RESULT 11

QB1C5 PRELIMINARY; PRT; 315 AA.
 ID QB1C5
 AC 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Predicted protein.
 GN MA230.

OS Methanomicrobia / ATCC 35395 / DSM 2834;
 OC Archaea; Burarchaeota; Methanococci; Methanomicrobiales;
 OC Methanococcaceae; Methanomicrobia.
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=21920760; Pubmed=1193238;
 RA Gajagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Attoor D., Brown A.,
 RA Allen N., Naylor J., Strange-Thomann N., Dearallano K., Johnson R.,
 RA Linton L., McElwain P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Heiderich R., Inglett-Smith C., Kuettner H.C., Krzycki J.A., Smith K.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., de Macario E.C.,
 RA Springer T.A., Umayam L.A., White R.H., Zinder S.H., Lander E.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RT "The genome of Methanomicrobia acetivorans reveals extensive metabolic
 and physiological diversity";
 RT Genome Res. 12:53-542(2002).
 RL EMBL; AB011134; AAM07575.1; -.
 KW Complete proteome; Sequence 315 AA; 34004 MN; 3649ABCBE8784486 CRC64;

Query Match 31.6%; Score 6; DB 17; Length 315;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPTSS 16
 Db 257 GGPTSS 262

RESULT 12

028129 PRELIMINARY; PRT; 364 AA.
 AC 028129;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

Query Match 31.6%; Score 6; DB 10; Length 411;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PTSEQ 18
 Db 134 PTSEQ 139

RESULT 13

09SH58 PRELIMINARY; PRT; 411 AA.
 ID 09SH58
 AC 09SH58
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DE F22012.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Spematophyta; Streptophyta; Embryophyta; Tracheophyta;
 OC eurosidids II; Brassicales; Brassicaceae; Arabidopsis.
 OC OXBOI_TAXID=3702;
 RN [1] SEQUENCE FROM N.A.
 RX Shinin P., Khan S., Brooks S., Buehler E., Chao Q., Dunn P., Kim C.,
 RA Walker M., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
 RA Hansen N.F., Huizar L., Kremenetskaya I., Lenz C., Li J., Liu S.,
 RA Luers S., Rowley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G.,
 RA Davis R.W., Fedderspiel N.A., Theologis A., Ecker J.R.,
 RT "Genomic sequence for Arabidopsis thaliana BAC F22C12 from chromosome
 RT I."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AAC07764; AAC24565.1; -.
 SQ Sequence 411 AA; 44511 MW; DA4EFD73C5D7797D CRC64;

Query Match 31.6%; Score 6; DB 10; Length 411;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PTSEQ 18
 Db 134 PTSEQ 139

RESULT 14

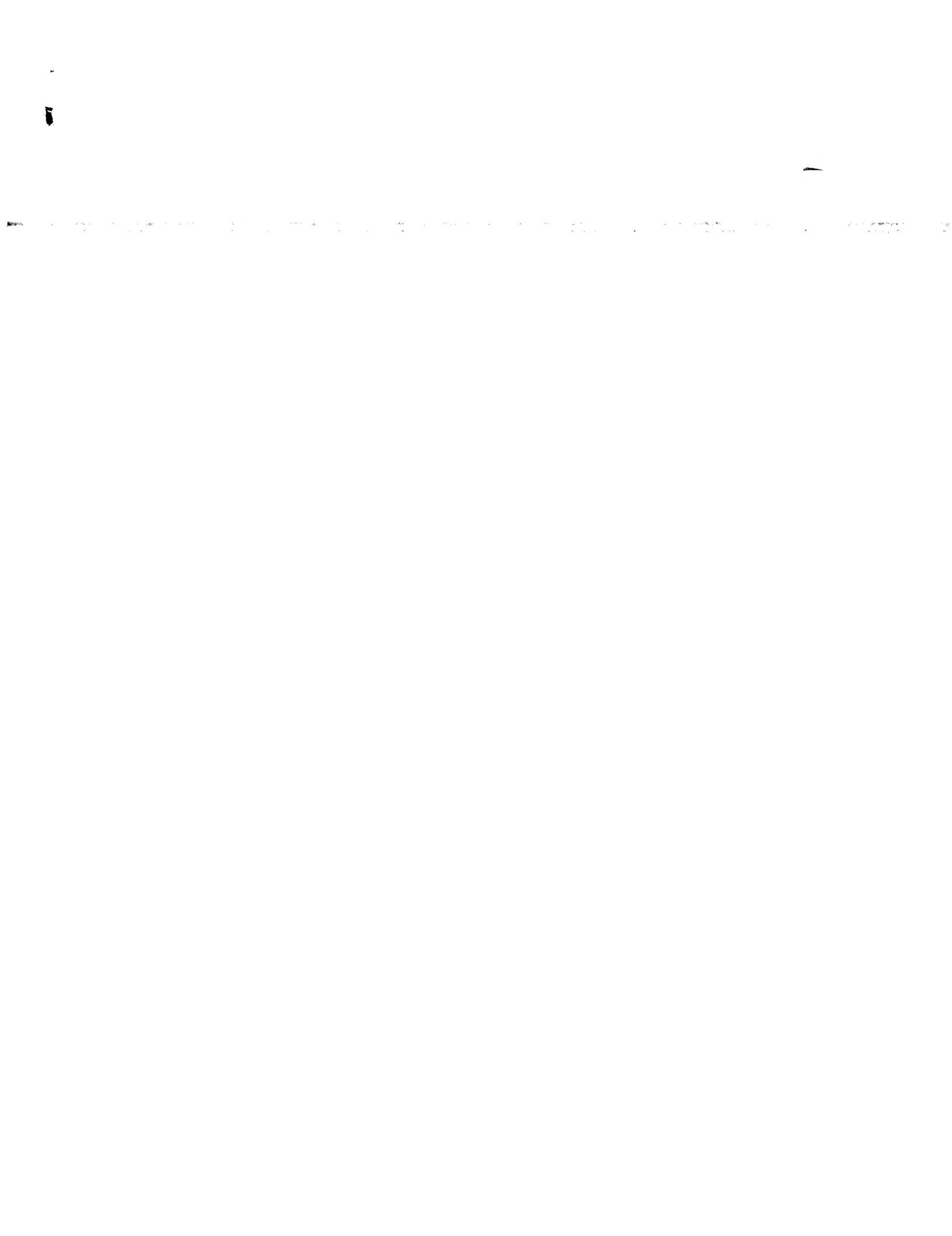
017816 PRELIMINARY; PRT; 447 AA.
 ID 017816
 AC 017816;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE C08B6_4 protein.
 GN C08B6_4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OX Rhabdiidae; Pelegderinae; Caenorhabditis.
 RN [1] NCBI_TaxID=6239;
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.;
 RL Submitted [MAY-1996] to the EMBL/GenBank/DDBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99069613; PubMed=9951916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for
 investigating biology";
 RL Science 282:2012-2018(1998);
 DR EMBL: Z72502; CA96587.1;
 DR HSSP; P23951; 2BAK.
 DR InterPro; IPR000726; Glyco_hydro_19.
 DR Pfam; PF00182; Glyco_hydro_19; 1.
 DR PRODOM; PD000574; Glyco_hydro_19; 1.
 SQ SEQUENCE 447 AA; 49583 MW; 6B4EC67A89B13D17 CRC64;
 Query Match 31.6%; Score 6; DB 5; Length 447;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GQPTSS 16
 Db 166 GQPTSS 171

RESULT 15

Q8Q880 PRELIMINARY; PRT; 504 AA.
 ID Q8Q880
 AC Q8Q880;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE pol protein (Fragment).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=00GAB-10K;
 RA Vergne L., Mitsoul I., Malonga-Mouillet G., Mavoungou R., Mansaray H.,
 RA Peeters M., Delaporte E.;
 RT "Emergence of HIV-1 drug-resistant variants in Gabon: need for
 implementation of guidelines on ARV use and drug resistance monitoring
 in developing countries.";
 RT J. Acquir. Immune Defic. Syndr. 0:0-0(2002).
 DR EMBL; AJ313412; CACB6073.1; -.
 FT NON_TER 1
 SQ SEQUENCE 604 AA; 68931 MW; BB07C9B6D30C4E62 CRC64;
 Query Match 31.6%; Score 6; DB 15; Length 604;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 PRSEQQ 18
 Db 25 PRSEQQ 30

Search completed: January 7, 2003, 12:39:49
 Job time : 26.359 secs



RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes";
 RL Neurosci. Lett. 220:183-186(1996).
 RN [3]
 RP SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=5129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x-long messenger ribonucleic acid levels.,";
 RL Endocrinology 136:232-241(1995).
 CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
 ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPlicing.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
 CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.
 CC
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 CC
 CC
 DR EMBL; U45729; AAC6327; 1;
 DR EMBL; U5918; AAC2998; 1;
 DR EMBL; U35098; AAA5200; 1;
 DR EMBL; S76511; AAC6700; 2;
 DR HSSP; P3553; 1AF3
 DR InterPro; IPR002475; BCL2_family.
 DR InterPro; IPR000712; Bcl12_BH.
 DR Pfam; PF00452; BCL-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 KW Apoptosis; Transmembrane; Alternative splicing.
 FT DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT CONFLICT 72 72 S -> N (IN REF. 3).
 FT CONFLICT 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).
 FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MW; /B3CD198D56DF589 CRC64;

47.4%; Score 9; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Pairs 0;

Db	11 GGPTSSEQI 19
RESULT 6	
BAXB_HUMAN	STANDARD; PRT; 218 AA.
ID Q07814;	
AC 007814;	
DT 01-FEB-1995 (Rel. 31, Created)	
DT 15-JUN-2002 (Rel. 41, last annotation update)	
DE Apoptosis regulator BAX_cytoplasmic isoform beta.	
GN BAX.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
[1]	
RP SEQUENCE FROM N.A.	
TISSUE=B cell;	
RX MEDLINE=93365978; PubMed=8358790;	
RA Oltrai Z.N., Millman C.L., Korsmeyer S.J.;	
CC "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death.,";	
RT Cell 74:609-619(1993).	
CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS	
CC HOMOLOG E1B 19K PROTEIN.	
CC -!- SUBUNIT: FORMS HOMODIMERS AND HETEROGENERS TOGETHER WITH BCL-2,	
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.	
CC -!- SUBCELLULAR LOCATION: Membrane-bound.	
CC -!- ALTERNATIVE PRODUCTS: A 21 kDa membrane-bound.	
CC -!- SIMILARITY: FORMS HOMODIMERS AND HETEROGENERS TOGETHER WITH BCL-2,	
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE CC SPlicing.	
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH CC HIGHEST LEVELS IN THE TESTIS AND OVARY.	
CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION	
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.	
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.	
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.	
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.	
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DR HSSP; Q07817; IMAZ.	
DR Genew; HNC_959; BAX.	
DR MIM_600040; /B3CD198D56DF589 CRC64.	
DR InterPro; IPR002475; BCL2_FAMILY.	
DR InterPro; IPR000712; Bcl12_BH.	
DR Pfam; PF00452; BCL-2; 1.	
DR SMART; SM00337; BCL; 1.	
DR PROSITE; PS01080; BH1; 1.	
DR PROSITE; PS01258; BH2; 1.	
DR PROSITE; PS01259; BH3; 1.	
DR PROSITE; PS50062; BCL2_FAMILY; 1.	
KW Apoptosis; Alternative splicing.	
FT DOMAIN 59 73 BH3.	
FT DOMAIN 98 118 BH1.	
FT DOMAIN 150 165 BH2.	
FT TRANSMEM 172 192 POTENTIAL.	
FT CONFLICT 72 72 S -> N (IN REF. 3).	
FT CONFLICT 76 76 L -> M (IN REF. 2).	
FT CONFLICT 126 126 C -> Y (IN REF. 2).	
FT CONFLICT 149 149 L -> F (IN REF. 3).	
FT CONFLICT 159 159 D -> E (IN REF. 1).	
SQ SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;	
Query Match 47.4%; Score 9; DB 1; Length 218;	
Best Local Similarity 100.0%; Pred. No. 0.0046;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Pairs 0;	
QY 11 GGPTSSEQI 19	

Matches 9; conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS01 19
| | | | |
ID 11 GGPTSS01 19

DR RESULT 7
YGRM_MICRO STANDARD; PRT: 105 AA.

ID YGRM_MICRO STANDARD; PRT: 105 AA.
AC P24621;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in GRM 3' region (Fragment).
OS Micromonospora rosea.
OC Bacteria; Actinobacteria; Actinomycetes; Micromonosporaceae;
OC Micromonospora; Micromonosporineae; Micromonosporaceae;
OC Micromonospora; Micromonosporaceae;
OK NCBI_TAXID=1878;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=91192615; PubMed=2013410;
RT "cloning and characterization of gentamicin-resistance genes from
Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:50 (1991).

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CC

DR EMBL; M55521; AAA25339.1; -.
DR PIR; P00018; PW0018.
KW Antibiotic resistance; Hypothetical protein.

FT NON_TER 105 AA; 11112 MW: 56125193440BA48C CRC64;
SQ SEQUENCE 11 105 AA: 11112 MW: 56125193440BA48C CRC64;
Query Match 31.6%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
| | | | |
DO 81 GOPTSS 86

RESULT 8
Y33K_HUMAN STANDARD; PRT: 298 AA.
ID Y33K_HUMAN STANDARD; PRT: 298 AA.
AC P04323;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN 2002 (Rel. 41, Last annotation update)
DE Hypothetical 33.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OK NCBI_TAXID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA POLLARD K.M.;
RT Submitted (JUN-1991) to the EMBL/Genbank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 1 UBA DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 UBX DOMAIN.

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CC

DR EMBL; M63123; AAA31522.1; -.
DR HSSP; P31109; LPCE.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002350; kazal.
DR Pfam; PF00050; kazal; 3.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM0200; KAZAL; 3.
DR PROSITE; PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 337
FOLLISTATIN.

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CC

CC EMBL; M88864; AAA36396.1; -.
DR InterPro; IPR000449; UBX_domain.
CC DR InterPro; IPR001012; UBX.
CC DR Pfam; PF00627; UBA; 1.
DR Pfam; PF00789; UBX; 1.
DR SMART; SM00166; UBA; 1.
DR SMART; SM00155; UBA; 1.
DR SMART; SM00166; UBX; 1.
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 33396 MW: 6C671CFF4A6C15D7 CRC64;
Query Match 31.6%; Score 6; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR 64 PTSS0 69

RESULT 9
FSA_SHEEP STANDARD; PRT: 337 AA.
ID FSA_SHEEP STANDARD; PRT: 337 AA.
AC P31514;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follistatin precursor (FS) (Activin-binding protein) (Fragment).
GN OS Ovis aries (Sheep).
CC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TAXID=9940;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=92331809; PubMed=1632897;
RT Tindall D.J., Hill D., Petersen G.B., Fleming J.S.:
"Ovine follistatin: characterization of cDNA and expression in sheep
ovary during the luteal phase of the oestrous cycle";
J. Mol. Endocrinol. 8:259-264 (1992).
CC -!- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).
CC -!- SUBUNIT: MONOMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC

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CC

DR EMBL; M63123; AAA31522.1; -.
DR HSSP; P31109; LPCE.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002350; kazal.
DR Pfam; PF00050; kazal; 3.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM0200; KAZAL; 3.
DR PROSITE; PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal.
FT NON_TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 337
FOLLISTATIN.

FT DOMAIN 87 110 FOLLISTATIN 1.
 FT DOMAIN 111 157 KAZAL-LIKE 1.
 FT DOMAIN 160 183 FOLLISTATIN 2.
 FT DOMAIN 185 232 KAZAL-LIKE 2.
 FT DOMAIN 237 261 FOLLISTATIN 3.
 FT DOMAIN 263 309 KAZAL-LIKE 3.
 FT DOMAIN 314 326 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DISUFIID 111 143 BY SIMILARITY.
 FT DISUFIID 115 136 BY SIMILARITY.
 FT DISUFIID 125 157 BY SIMILARITY.
 FT DISUFIID 185 218 BY SIMILARITY.
 FT DISUFIID 189 211 BY SIMILARITY.
 FT DISUFIID 200 232 BY SIMILARITY.
 FT DISUFIID 263 295 BY SIMILARITY.
 FT DISUFIID 267 288 BY SIMILARITY.
 FT DISUFIID 277 309 BY SIMILARITY.
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 337 AA; 37082 MW; 1B8BE1BB6B109C4 CRC64;
 Query Match 31.6%; Score 6; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred No 12; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 13 PTSSEQ 18
 Db 192 PTSSEQ 197

RESULT 10
 FSA_BOVIN STANDARD PRT: 344 AA.
 AC P50291; ID FSA_BOVIN
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Follistatin precursor (FSS) (Activin-binding protein).
 FN FST
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=Holstein; TISSUE=Testicle, and Ovary;
 RX MEDLINE=94280841; PUBMED=8011323;
 RA Houda A., Lussier J.G., Ethier J.F., Gagnon C., Silversides D.W.,
 RT "Cloning and tissue expression of bovine follistatin cDNA.",
 Mol. Reprod. Dev. 37:391-397(1994).
 !- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
 ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
 OF PITUITARY POLYLCLE STIMULATING HORMONE (FSH).
 !- SUBUNIT: MONOMER (POTENTIAL).
 !- SUBCELLULAR LOCATION: Secreted.
 !- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.

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CC EMBL; L2116; AAA0522.1; -.
 DR HSSP; P37109; IPCE.
 DR InterPro; IPRO03645; F0JN.
 DR InterPro; IPRO02350; kazal.
 DR Pfam; PF00050; kazal; 3.
 DR SMART; SM00274; F0JN; 3.
 DR SMART; SM00280; KAZAL; 3.

DR PROSITE; PS00082; KAZAL; FALSE_NEG.
 KW Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 344 FOLLISTATIN.
 FT DOMAIN 94 117 FOLLISTATIN 1.
 FT DOMAIN 118 164 KAZAL-LIKE 1.
 FT DOMAIN 157 190 FOLLISTATIN 2.
 FT DOMAIN 192 239 KAZAL-LIKE 2.
 FT DOMAIN 244 268 FOLLISTATIN 3.
 FT DOMAIN 270 316 KAZAL-LIKE 3.
 FT DISUFIID 118 150 BY SIMILARITY.
 FT DISUFIID 122 143 BY SIMILARITY.
 FT DISUFIID 132 164 BY SIMILARITY.
 FT DISUFIID 192 225 BY SIMILARITY.
 FT DISUFIID 218 218 BY SIMILARITY.
 FT DISUFIID 207 239 BY SIMILARITY.
 FT DISUFIID 270 302 BY SIMILARITY.
 FT DISUFIID 274 295 BY SIMILARITY.
 FT DISUFIID 284 316 BY SIMILARITY.
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 344 AA; 37959 MW; 01B8EE8A84F8710 CRC64;
 Query Match 31.6%; Score 6; DB 1; Length 344;
 Best Local Similarity 100.0%; Pred No 13; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 13 PTSSEQ 18
 Db 199 PTSSEQ 204

RESULT 11
 FSA_HORSE STANDARD PRT: 344 AA.
 AC P62050; ID FSA_HORSE
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE Follistatin precursor (FSS) (Activin-binding protein).
 FN FST
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollicle;
 RX MEDLINE=99261574; PUBMED=10331189;
 RA Sugawara Y., Yamamoto K., Naito K., Tachi C., Tojo H., Sawasaki T.;
 RT "Molecular cloning of cDNA for equine follistatin and its gene
 expression in the reproductive tissues of the mare.";
 RL J. Vet. Med. Sci. 61:201-207(1999).
 !- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
 ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
 OF PITUITARY POLYLCLE STIMULATING HORMONE (FSH).
 !- SUBUNIT: MONOMER (POTENTIAL).
 !- SUBCELLULAR LOCATION: Secreted.
 !- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

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 CC EMBL; AB010829; BAA25699.1; -.
 DR HSSP; P37109; IPCE.
 DR InterPro; IPRO03645; F0JN.
 DR InterPro; IPRO02350; kazal.

[2] RQ STRAIN=Cv. Landsberg erecta;
 SEQUENCE FROM N.A.
 RA MEDLINE=938446005; PubMed=681027;
 RA RX
 RA Taylor R.M.; Hamer M.J.; Rosenthal J.; Bray C.M.;
 RA "Molecular cloning and functional analysis of the Arabidopsis
 RL Submitted (MARR-1994) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=93173125; PubMed=8437590;
 RA Chen P.C.; Lee K.S.; Levin D.E.;
 RA "A pair of putative protein kinase genes (YPK1 and YPK2) is required
 RT for cell growth in *Saccharomyces cerevisiae*.";
 RL Mol. Gen. Genet. 236:433-447(1993);
 CC -!- FUNCTION: PLAYS AN ESSENTIAL ROLE IN THE PROLIFERATION OF YEAST
 CC CELLS.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY: STRONGEST TO YPK2.
 CC -----
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 CC -----
 DR EMBL: M21307; AAA34880_1; -.
 DR EMBL; 228126; CAB81967_1; -.
 DR PIR: S37955; S37955.
 DR HSSP; P05132; ICP.
 DR SGD; S0001609; YPK1.
 DR InterPro: IPR000719; Euk_pk kinase.
 DR InterPro: IPR00961; Pkinase_C.
 DR InterPro: IPR002250; Ser_thr_pk kinase.
 DR Pfam; PF00059; kinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRODOM; PD000001; Euk_pk kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK_C; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transf erase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 347 602 PROTEIN KINASE.
 FT NP_BIND 553 361 ATP (BY SIMILARITY).
 FT BINDING 576 376 ATP (BY SIMILARITY).
 FT ACT_SITE 570 470 BY SIMILARITY
 FT CONFLICT 201 201 P -> L (IN REF. 2).
 FT CONFLICT 553 553 M -> I (IN REF. 2).
 SQ 680 AA; 7647 MW; 00112BBB849CDD2B5 CRC64;
 Qy 14 TSSEQI 19
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 Db 764 TSSEQI 769

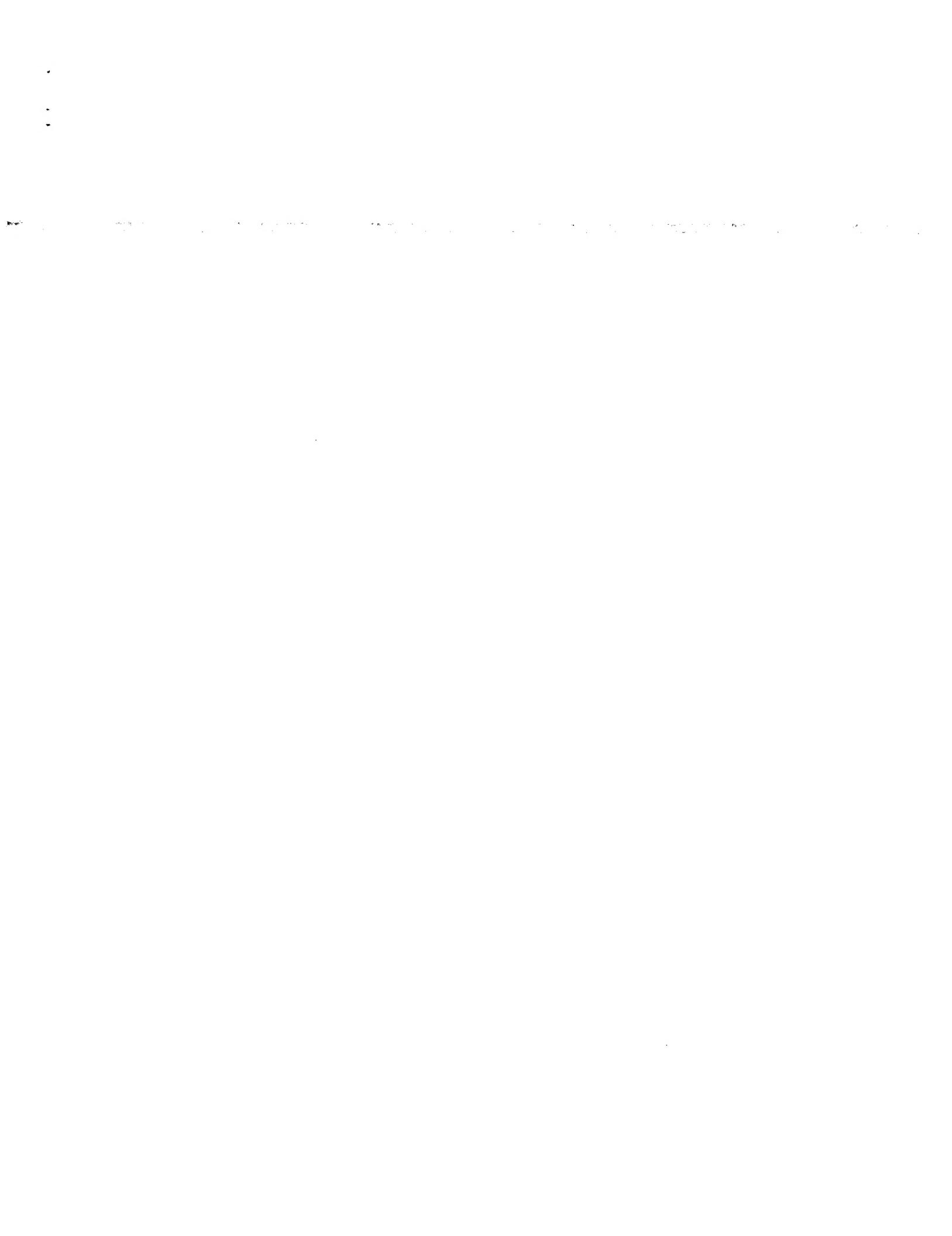
 RESULT 15
 ID IRBP_HUMAN
 ID IRBP_HUMAN STANDARD; PRT; 1247 AA.
 AC P10745;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interphotoreceptor retinoid-binding protein precursor (IRBP)
 DE (Interstitial retinol-binding protein).
 DE RBP3.
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89355256; PubMed=2542268;
 RA Liou G.I.; Ma D.-P.; Yang Y.-W.; Geng L.; Zhu C.; Baehr W.;
 RA "Human interstitial retinoid-binding protein. Gene structure and
 RT primary structure.";
 RT *J. Biol. Chem.* 264:8220-8226(1989).
 RN [2]
 SEQUENCE FROM N.A.
 RX MEDLINE=90154038; PubMed=2303470;
 RA Fong S.-L.; Fong W.B.; Morris T.A.; Kedzie K.M.; Bridges C.D.B.;
 RA "Characterization and comparative structural features of the gene for
 RT human interstitial retinol-binding protein.";
 RT Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 RN J. Biol. Chem. 265:3648-3653(1990).
 RN [3]
 SEQUENCE FROM N.A.
 RX MEDLINE=90006790; PubMed=2792773;
 RA SI J.S.; Borst D.E.; Redmond T.M.; Nickerson J.M.;
 RP SEQUENCE FROM N.A.

RT "Cloning of cDNAs encoding human interphotoreceptor retinoid-binding protein (IRBP) and comparison with bovine IRBP sequences"; -
 RT Gene; HGNC:9921; RBP3.
 RT MIM: 180290; -.
 RT InterPro: IPR003581; TSPC.
 DR Pfam: PF02692; IRBP; 4.
 DR SMART: SM00245; TSPC; 4.
 RP RX Viamin A; Transport; Repeat; Signal; Glycoprotein.
 KW FT SIGNAL 1 17
 RP FT CHAIN 18 1247 INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN.
 RA Bridges C.D.B.;
 RA Christie S., Rout D., Bhattacharya S., Cook R.G., Li Y., Wang C.,
 RT "human interstitial retinol-binding protein (IRBP): cloning, partial sequence, and chromosomal localization.";
 RT Somat. Cell Mol. Genet. 13:315-323(1987).
 RL J. BIOL. CHEM. 263:15330-15334(1988).
 RN [5]
 RP MEDLINE=89008429; PubMed=3170584;
 RA Fong S.-L., Bridges C.D.B.;
 RT "Internal quadruplication in the structure of human interstitial retinol-binding protein deduced from its cloned cDNA.>";
 RL J. BIOL. CHEM. 263:15330-15334(1988).
 RN [6]
 RP SEQUENCE OF 1-382 FROM N.A.
 RA Albinia A., Toffenetti J., Zhen Z., Chader G.J., Noonan D.M.;
 RT "Hypomethylation of the interphotoreceptor retinoid-binding protein (IRBP) promoter and first exon is linked to expression of the gene.>";
 RL Nucleic Acids Res. 18:5181-5187(1990).
 RN [7]
 RP SEQUENCE OF 18-42.
 RA MEDLINE=87156570; PubMed=3827838;
 RA Redmond T.M., Wiggett B., Robey F.A., Chader G.J.;
 RT "Interspecies conservation of structure of interphotoreceptor retinoid-binding protein. Similarities and differences as adjudged by peptide mapping and N-terminal sequencing.";
 RL Biochem. J. 240:19-26(1986).
 RN [8]
 RP SEQUENCE OF 23-39.
 RX MEDLINE=86301171; PubMed=1743780;
 RA Fong S.-L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:319-312(1986).
 -! FUNCTION: IRBP SHUTTLES 11-CTS AND ALL TRANS RETINOLDS BETWEEN THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 -! SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT EPITHELIUM CELLS.
 CC -! CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-2 IS THE INITIATOR.
 CC ! CAUTION: REF.4 AND REF.5 SEQUENCES HAVE BEEN SHOWN TO BE INCORRECT
 CC AND THE REVISED SEQUENCE IS GIVEN IN REF.1, REF.2 AND REF.3.
 CC
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Query	Match	Score	Length	Best local	Similarity	Pred.	Matches	Conservative	Mismatches	Indels	Gaps
OY	11	GGPTSS	16		31.6%	6	DB 1	100.0%	0	0	0
Db	1086	GGPTSS	1091								

Search completed: January 7, 2003, 12:38:52
 Job time : 8.82051 secs

DR Gene; HGNC:9921; RBP3.
 DR MIM: 180290; -.
 DR InterPro: IPR003581; TSPC.
 DR Pfam: PF02692; IRBP; 4.
 DR SMART: SM00245; TSPC; 4.
 DR Viamin A; Transport; Repeat; Signal; Glycoprotein.
 KW FT SIGNAL 1 17
 DR FT CHAIN 18 1247 INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN.
 DR DOMAIN 18 1230 4 X APPROXIMATE TANDEM REPEATS.
 DR FT REPEAT 18 320 1.
 DR REPEAT 321 630 2.
 DR REPEAT 631 931 3.
 DR REPEAT 932 1230 4.
 DR REPEAT 205 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL). CARBOHYD
 DR FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
 DR FT SEQUENCE 1247 AA; 135362 MW; 6C1B41411EB012EOF CRC64;



Copyright (c) 1993 - 2003 CompuGen Ltd.	GenCore version 5.1.3			
OM protein - protein search, using sw model				
Run on: January 7, 2003 ; Search time 12.6667 seconds	(without alignments)			
Scoring table: OLIGO	144.202 Million cell updates/sec			
Searched: 283224 seqs, 96134422 residues				
Word size : 0				
Total number of hits satisfying chosen parameters: 283224				
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Post-processing: Listing first 45 summaries				
Database : PIR_73;*				
1: pir1;*				
2: pir2;*				
3: pir3;*				
4: pir4;*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result NO.	Score	Query Match Length	DB ID	Description
-----		-----		
1	9	47.4	I38921	bcl-2-associated protein x, delta splice form - human
2	9	47.4	JC7255	Bax delta protein
3	9	47.4	A47538	bcl-2-associated p
4	9	47.4	D47538	bcl-2-associated p
5	9	47.4	B47538	bcl-2-associated p
6	6	31.6	PW0018	hypothetical prote
7	6	31.6	105	interphotoreceptor
8	6	31.6	298	hypothetical prote
9	6	31.6	304	interphotoreceptor
10	6	31.6	337	folistatin - sheep
11	6	31.6	344	folistatin - precursor
12	6	31.6	344	folistatin - bovi
13	6	31.6	364	folistatin - human
14	6	31.6	411	interstitial retin
15	6	31.6	441	protein F22C2.16
16	6	31.6	447	retinol-binding pr
17	6	31.6	680	hypothetical prote
18	6	31.6	790	protein kinase YPK
19	6	31.6	1028	DNA ligase (ATP) (
20	6	31.6	1028	BIG-1 protein - rat
21	6	31.6	1148	plasmacytoma-assoc
22	6	31.6	1247	probable calcineurin c
23	6	31.6	1286	interphotoreceptor
24	6	31.6	1576	interphotoreceptor
25	6	31.6	2165	homoeotic protein H
26	6	31.6	2245	genome polyprotein
27	5	26.3	41	myrosin heavy chain
28	5	26.3	53	bcl-2-associated p
29	5	26.3	H82571	hypothetical prote
				C:Keywords: transmembrane protein
ALIGNMENTS				
Query Match	47.4%	Score	9;	DB 2; length 143;
Matches	9;	Local Similarity	100.0%;	Pred. No. 0.0055;
QY	11	GGPTSSEQI	19	Mismatches 0; Indels 0; Gaps 0;
Db	111	GGPTSSEQI	19	
RESULT 1				
I38921				
bcl-2-associated protein x, delta splice form - human				
N:Alternative names: BAX; programmed cell death membrane protein x delta				
C:Species: Homo sapiens (man)				
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000				
C:Accession: I38921				
R:Apte, S.S.; Mattei, M.G.; Olsen, B.R.				
Gentics 26, 592-594, 1995				
A;Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a				
A;Reference number: I38921; MUID:95331797; PMID:7607685				
A;Accession: I38921				
A;Status: preliminary; nucleic acid sequence not shown; translation not shown .				
A;Molecule type: mRNA				
A;Residues: 1-143 <RES>				
A;Cross references: EMBL:U19599; NID:9841237; PIDN: AAC50142.1; PID:9841238				
C:Genetics:				
A;Gene: GDB:BAX				
A;Cross references: GDB:228082; OMIM:600040				
A;Map position: 19q13.3-19q13.4				
C:Superfamily: bcl transforming protein				
RESULT 2				
JC7255				
Bar-delta protein - human				
C:Species: Homo sapiens (man)				
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000				
C:Accession: JC7255				
R:Schmitz, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.				
Biochem. Biophys. Res. Commun. 270, 868-879, 2000				
A;Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.				
A;Reference number: JC7255				
A;Accession: JC7255				
A;Molecule type: mRNA				
A;Residues: 1-179 <SCH>				
A;Cross references: GB:AF247393				
A;Experimental source: cancer promyelocytic cells				
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It				
C:Superfamily: bcl transforming protein				
Query Match	47.4%	Score	9;	DB 2; length 179;

Best local Similarity 100.0%; Pred. No. 0.0068; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; MisMatches 0;

**Qy 11 GGPNSSEQI 19
Db 11 GGPNSSEQI 19**

RESULT 3

A47538

bcl-2-associated protein x, alpha splice form - human
N; alternate names: BAX; programmed cell death membrane protein x alpha
C; species: Homo sapiens (man)
C; date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C; accession: A47538
R; Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A; title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A; reference number: A47538
A; accession: B47538
A; molecule type: mRNA
A; residues: 1-192 <OLT>
A; note: the amino end of the mature protein is blocked
A; cross-references: GDB:228082; OMIM:600040
A; map position: 19q13.3-19q13.4
C; superfamily: bcl transforming protein
C; keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembrane F; 172-191/Domain: transmembrane #status predicted <XML>

Query Match 47.4%; Score 9; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0073; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPNSSEQI 19
Db 11 GGPNSSEQI 19

RESULT 4

D47538

bcl-2-associated protein x - mouse
N; alternate names: BAX; programmed cell death membrane protein x
C; species: Mus musculus (house mouse)
C; date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C; accession: D47538
R; Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
A; title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A; reference number: A47538; MUID:93364978; PMID:8358790
A; accession: D47538
A; status: preliminary
A; molecule type: mRNA
A; residues: 1-192 <OLT>
A; cross-references: GB:L22472
C; genetics:
A; gene: bax
C; superfamily: bcl transforming protein

Query Match 47.4%; Score 9; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0073; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPNSSEQI 19
Db 11 GGPNSSEQI 19

RESULT 5

Ba7538

bcl-2-associated protein x, beta splice form - human
N; alternate names: BAX; programmed cell death membrane protein x alpha
C; species: Homo sapiens (man)
C; date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C; accession: B47538
R; Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A; title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A; reference number: A47538; MUID:93364978; PMID:8358790
A; accession: B47538
A; molecule type: mRNA
A; residues: 1-218 <OLT>
A; cross-references: GB:L22474; MUID:9388167; PIDN:AAA03620_1; PID:9388168
A; map position: 19q13.3-19q13.4
C; superfamily: bcl transforming protein
C; keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer
Query Match 47.4%; Score 9; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0082; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPNSSEQI 19
Db 11 GGPNSSEQI 19

RESULT 6

PW0018

hypothetical protein 105 - Micromonospora sp. (fragment)
C; species: Micromonospora sp.
C; date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C; accession: PW0018
R; Kleijnen, G.H.; Gundliffe, B.; Finansek, I.
Gene 98, 53-60, 1991
Cell 74, 609-619, 1993
A; title: Cloning and characterization of gentamicin-resistance genes from Micromonospora
A; reference number: JG0017; MUID:91192615; PMID:2013410
A; accession: PW0018
A; molecule type: DNA
A; residues: 1-105 <KEL>
A; cross-references: GB:M5527
A; note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a
Query Match 31.6%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.6; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 11 GGPNSS 16
Db 81 GGPNSS 86

RESULT 7

S33927

interphotoreceptor retinoid-binding protein - African clawed frog (fragment)
C; species: Xenopus laevis (African clawed frog)
C; date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C; accession: S33927
R; Gonzalez-Fernandez, F.; Kittredge, K.L.; Rayborn, M.E.; Hollyfield, J.G.; Landers, J. Cell Sci. 105, 7-21, 1993
A; title: Interphotoreceptor retinoid-binding protein (IRBP), a major 124 kDa glycoprotein
A; reference number: S33927; MUID:93366942; PMID:8360278
A; accession: S33927
A; status: preliminary
A; molecule type: DNA
A; residues: 1-297 <GON>
A; cross-references: EML:X69469; MUID:9313172; PIDN:CAA49228_1; PID:9313173
C; superfamily: interphotoreceptor retinoid-binding protein
C; keywords: duplication

Query Match 31.6%; Score 6; DB 2; Length 297;

RESULT 5

Ba7538

bcl-2-associated protein x, beta splice form - human
N; alternate names: BAX; programmed cell death membrane protein x alpha
C; species: Homo sapiens (man)
C; date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C; accession: B47538
R; Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A; title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A; reference number: A47538; MUID:93364978; PMID:8358790
A; accession: B47538
A; molecule type: mRNA
A; residues: 1-218 <OLT>
A; cross-references: GB:L22474; MUID:9388167; PIDN:AAA03620_1; PID:9388168
A; map position: 19q13.3-19q13.4
C; superfamily: bcl transforming protein
C; keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer
Query Match 47.4%; Score 9; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0082; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPNSSEQI 19
Db 11 GGPNSSEQI 19

Best Local Similarity 100.0%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C-Species: ovis orientalis aries, ovis ammon aries (domestic sheep)

Qy 11 GGPTSS 16
Db 146 GGPTSS 150

RESULT 8
S27965
C;Species: Homo sapiens (man)
C;Date: 7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Sep-2000
C;Accession: S27965
R;Pollard, K. M.
Submitted to the EMBL Data Library, June 1991
A;Reference number: S27965
A;Accession: S27965
A;Molecule type: mRNA
A;Residues: 1-298 <POI>
A;Cross-references: EMBL:68864; NID:9189396; PIDN:AAA36396_1; PID:9189397
C;Superfamily: Caenorhabditis elegans hypothetical protein F23C8.4

Query Match 31.6%; Score 6; DB 2; Length 337; Best Local Similarity 100.0%; Pred. No. 25; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C-Species: Rattus norvegicus (Norway rat)

Qy 13 PRSSEQ 18
Db 64 PRSSEQ 69

RESULT 9
A49185
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C;Accession: A49185
R;Gonzalez-Fernandez, F.; van Niel, E.; Edmonds, C.; Beaver, H.; Nickerson, J.M.; Garcia EXP. Eye Res. 56, 411-427, 1993
A;Title: Differential expression of interphotoreceptor retinoid-binding protein, opsin, A;Reference number: A49185; MUID:9372869; PMID:7916695
A;Accession: A49185
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-304 <GO>
A;Note: sequence extracted from NCBI backbone (NCBIN:133270, NCBIPI:133271)
C;Superfamily: interphotoreceptor retinoid-binding protein
C;Keywords: duplication

Query Match 31.6%; Score 6; DB 2; Length 304; Best Local Similarity 100.0%; Pred. No. 23; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C-Species: ovine follistatin - sheep (fragment)

Qy 11 GGPTSS 16
Db 154 GGPTSS 159

RESULT 10
I47079
C;Species: ovine follistatin - sheep (fragment), ovis ammon aries (domestic sheep)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 20-Apr-2001
C;Accession: I47079
R;Tisdall, D.J.; Hill, D.; Petersen, G.B.; Fleming, J.S.
J. Mol. Endocrinol. 8, 259-264, 1992
A;Title: Ovine follistatin: characterization of cDNA and expression in sheep ovary during
A;Reference number: I47079; MUID:92337809; PMID:1632897
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-337 <TTS>

RESULT 11
A27701
folistatin precursor - pig
N;contains: follistatin short form precursor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-2000
C;Accession: A27701; A40064; B40064; A39969; A47139
R;Shimasaki, S.; Koga, M.; Esch, F.; Mercado, M.; Cooksey, K.; Koba, A.; Ling, N. Biochem. Biophys. Commun. 152, 71-723, 1988
A;Title: Porcine follistatin gene structure supports two forms of mature follistatin
A;Reference number: A27701; MUID:88209050; PMID:3365249
A;Accession: A27701
A;Molecule type: DNA
A;Residues: 1-344 <SH1>
A;Cross-references: GB:M19529; NID:9164458; PIDN:AAA31036_1; PID:9164459
R;Esch, F.S.; Shimasaki, S.; Mercado, M.; Cooksey, K.; Ling, N.; Ying, S.; Ueno, N.; Mol. Endocrinol. 1, 849-855, 1987
A;Title: Structural characterization of follistatin: a novel follicle-stimulating hor
A;Reference number: A40064; MUID:91042571; PMID:3153465
A;Accession: A40064
A;Molecule type: mRNA
A;Residues: 1-344 <ESG1>
A;Cross-references: GB:M36512; GB:M36513; NID:9164461
A;Accession: B40064
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-317 <ESG2>
A;Cross-references: GB:M36512; GB:M36513; NID:9164461
R;Ueno, N.; Ling, N.; Ying, S.Y.; Esch, F.; Shimasaki, S.; Guillemin, R. Proc. Natl. Acad. Sci. U.S.A. 84, 8282-8286, 1987
A;Title: Isolation and partial characterization of follistatin: a single-chain M-r 35
A;Reference number: A39969; MUID:88068578; PMID:3120188
A;Accession: A39969
A;Molecule type: protein
A;Residues: 30-37 <UEN>
R;Sugino, K.; Kurasawa, N.; Nakamura, T.; Takio, K.; Shimasaki, S.; Ling, N.; Titani, J. Biol. Chem. 268, 15579-15587, 1993
A;Title: Molecular heterogeneity of follistatin, an activin-binding protein. Higher a
A;Reference number: A47139; MUID:9330158; PMID:830384
A;Accession: A47139
A;Status: preliminary
A;Molecule type: protein
A;Residues: 30-37; I20128; 284-292; 312-344 <SUG>
C;Comment: Follistatin inhibits release of pituitary follicle stimulating hormone.
C;Genetics:
A;Introns: 29/1; 93/1; 166/1; 241/1; 318/1
C;Superfamily: follistatin; Kazal protease inhibitor homology
C;Keywords: alternative splicing; glycoprotein; monomer
F;1-29(Domain: signal sequence #status predicted <SIG>
F;30-34/Product: follistatin #status predicted <MAS>
F;30-34/Product: follistatin, short splice form #status predicted <MAS>
F;114-164/Domain: Kazal protease inhibitor homology <RP18>
Query Match 31.6%; Score 6; DB 1; Length 344; Best Local Similarity 100.0%; Pred. No. 26; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C-Species: follistatin inhibitor homology <RP18>

Qy 13 PRSSEQ 18
Db 192 PRSSEQ 197

A;Cross-references: GB:M63123; NID:9165882; PIDN:AAA31522_1; PID:9165883
C;Superfamily: follistatin; Kazal protease inhibitor homology
F;107-157/Domain: Kazal protease inhibitor homology <RP1>
F;181-232/Domain: Kazal protease inhibitor homology <RP12>
F;258-309/Domain: Kazal protease inhibitor homology <RP13>

Db	199	PTSSSEQ	204
RESULT	12		
I45894		folistatin - bovine	
C;Species:	Bos primigenius taurus (cattle)		
C;Date:	15-Oct-1996	#sequence_revision 15-Oct-1996	#text_change 17-Nov-2000
C;Accession:	I45894		
R;Houde,	A.; Lussier, J.-G.; Ethier, J.F.; Gagnon, C.; Silversides, D.W.		
Mol.	Reprod. Dev	37', 391-397,	1994
A;Title:	Cloning and tissue expression of bovine follistatin cDNA.		
A;Reference number:	I45894;	MUID:94280841;	PMID:8011323
A;Status:	preliminary;	translated from GB/EMBL/DBJ	
A;Molecule type:	mRNA		
A;Residues:	1-344 <HOU>		
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Vision Res.	26,	1645-1653,	1986
A;Title:	Bovine interstitial retinol-binding protein (IRBP)-isolation and sequence analysis		
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C;Date:	02-Mar-2001	#sequence_revision 02-Mar-2001	#text_change 31-Mar-2001
R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.H.; Chung, C.W.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hugues, B.; Hulzar, L.			
Nature	408,	816-820,	2000
A;Authors:	Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.		
Search completed: January 7, 2003, 12:40:22			
Job time : 14.6667 secs			

ON protein - protein search, using sw model

Run on : January 7, 2003, 12:38:59 ; Search time 11.2051 Seconds
 (without alignments)
 120.181 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

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Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 262191 seqs, 70875818 residues

Word size : 0

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Pending Patents AA_New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	9	47.4	192	1	PCT-US02-38191-5
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4	9	47.4	192	1	PCT-US02-32727-10714
5	6	31.6	94	6	US-10-057-498-10714
6	6	31.6	120	6	US-10-092-411A-5332
7	6	31.6	586	6	US-10-258-951-54
8	6	31.6	748	1	US-09-134-000C-6041
9	6	31.6	4219	6	US-10-085-198-2
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12	5	26.3	49	6	US-10-203-138A-13021
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods for Identifying Modulators of
; FILE REFERENCE: P-LU 5535
; CURRENT APPLICATION NUMBER: US/10/306,878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; NUMBER OF SEQ ID NOS: 28
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US-10-306-878-5

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; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhattacharya, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siping
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: PCT-US02-32727-10714
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; APPLICANT: Mitcham, Jennifer
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; APPLICANT: Persing, David
; APPLICANT: Bhattacharya, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siping
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; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
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; APPLICANT: Lynn Doucette Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCAL EPITHELMIDES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 03/2196-101
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; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
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; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
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; GENERAL INFORMATION:

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APPLICANT: Agarwal, Pankaj
 APPLICANT: Murdock, Paul R.
 APPLICANT: Rizvi, Safia K.
 APPLICANT: Smith, Randall F.
 APPLICANT: Xiang, Zhaoying
 APPLICANT: Kabnick, Karen
 APPLICANT: Lai, Ying-Ta
 APPLICANT: Xie, Qing
 TITLE OF INVENTION: NOVEL COMPOUNDS
 FILE REFERENCE: GP0025
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 CURRENT FILING DATE: 2002-10-28
 PRIOR APPLICATION NUMBER: PCT/US01/13360
 PRIOR FILING DATE: 2001-04-26
 PRIOR APPLICATION NUMBER: 60/199,963
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 60/203,336
 PRIOR FILING DATE: 2000-05-11
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 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134 000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 6041
 ; LENGTH: 748
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-6041

Query Match 31.6%; Score 6; DB 5; Length 748;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
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 Db 1549 GGPTSS 1554

RESULT 10
 US-10-308-128-65
 ; Sequence 65, Application US/10308128
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN MITOCHONDRIAL AND MICROSOFT
 ; TITLE OF INVENTION: GLYCEROL-3-PHOSPHATE ACYLTRANSFERASES AND VARIANTS THEREOF
 ; FILE REFERENCE: D0199 NP
 ; CURRENT APPLICATION NUMBER: US/10/308,128
 ; CURRENT FILING DATE: 2002-12-02
 ; PRIOR APPLICATION NUMBER: U.S. 60/334,904
 ; PRIOR FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 205
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 65
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-308-128-65

Query Match 26.3%; Score 5; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 91; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 15
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 Db 6 GGPTSS 10

RESULT 11
 US-10-085-198-2
 ; Sequence 2, Application US/10085198
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook et al.

Sequence 298, Application US/60427045
 GENERAL INFORMATION:
 APPLICANT: The Board of Trustees of the University of Arkansas
 APPLICANT: O'Brien, Timothy
 APPLICANT: Beard, John
 APPLICANT: Underwood, Lowell
 TITLE OF INVENTION: CA125 Gene and its Use for Diagnostic and Therapeutic Interventions
 FILE REFERENCE: 022438.44514
 CURRENT APPLICATION NUMBER: US/60/427,045
 CURRENT FILING DATE: 2002-11-15
 NUMBER OF SEQ ID NOS: 314
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 298
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Homo sapiens
 US 60-427-045-298

RESULT 12
 US-10-203-138A-13021
 Sequence 13021, Application US/10203138A
 GENERAL INFORMATION:
 APPLICANT: Molecular Dynamics, Inc.
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN BT 474
 FILE REFERENCE: PB 0004 WO 8
 CURRENT APPLICATION NUMBER: US/10/203,138A
 CURRENT FILING DATE: 2002-08-02
 PRIOR APPLICATION NUMBER: US 60/180,312 (04.02.00)
 PRIOR FILING DATE: 04 February 2000 (04.02.00)
 PRIOR APPLICATION NUMBER: US 60/207,456 (26.05.00)
 PRIOR FILING DATE: 26 May 2000 (26.05.00)
 PRIOR APPLICATION NUMBER: US 09/632,366 (03.08.00)
 PRIOR FILING DATE: 03 August 2000 (03.08.00)
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 03 October 2000 (03.10.00)
 PRIOR APPLICATION NUMBER: US 60/235,359 (27.09.00)
 PRIOR FILING DATE: 27 September 2000 (27.09.00)
 PRIOR APPLICATION NUMBER: US 60/234,687 (21.09.00)
 PRIOR FILING DATE: 21 September 2000 (21.09.00)
 PRIOR APPLICATION NUMBER: US 09/608,408 (30.06.00)
 NUMBER OF SEQ ID NOS: 15/38
 SOFTWARE: Molecular Dynamics Sequence Listing Engine
 SEQ ID NO 13021
 LENGTH: 49
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL109942.4
 FEATURE:
 OTHER INFORMATION: EXPRESSED IN BI474, SIGNAL = 2.3
 FEATURE:
 OTHER INFORMATION: OTHER INFORMATION: EST_HUMAN HIT: BE707262.1, EVALUE 3.90e+00
 US-10-203-138A-13021
 Query Match 26.3%; Score 5; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-10-213-102-365
 Sequence 365, Application US/10218102
 GENERAL INFORMATION:
 APPLICANT: Bentzen, Joerg
 APPLICANT: Dahiyat, Bassil I.
 APPLICANT: Desarlais, John R.
 APPLICANT: Hayes, Robert J.
 APPLICANT: Vielmetter, Jost
 TITLE OF INVENTION: Protein Design Automation for Protein Libraries
 FILE REFERENCE: A 6/229-11/RFT/RMS/RMK
 CURRENT APPLICATION NUMBER: US/10/218,102
 PRIOR APPLICATION NUMBER: US 09/927,790
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: US 60/311,545
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: US 60/324,899
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/351,937
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: US 60/352,103
 PRIOR FILING DATE: 2002-01-25
 NUMBER OF SEQ ID NOS: 432
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 365
 LENGTH: 49
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: synthetic
 US-10-213-102-365

RESULT 14
 PCT-US02/32727-19622
 Sequence 19622, Application PC/US02/32727
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer
 APPLICANT: Skeiky, Yasli
 APPLICANT: Persing, David
 APPLICANT: Bhakta, Ajay
 APPLICANT: Maisonneuve, Jean Francois
 APPLICANT: Zhang, Yanni
 APPLICANT: Wang, Siqing
 APPLICANT: Jen, Shyan
 APPLICANT: Lodes, Michael
 APPLICANT: Benson, Darin
 APPLICANT: Jones, Robert
 APPLICANT: Carter, Darrick
 APPLICANT: Barth, Brenda
 APPLICANT: Douglass, John
 TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 FILE REFERENCE: 210121.514C1
 CURRENT APPLICATION NUMBER: PCT/US02/32727
 CURRENT FILING DATE: 2002-10-11
 NUMBER OF SEQ ID NOS: 30992
 SEQ ID NO 19622
 LENGTH: 50

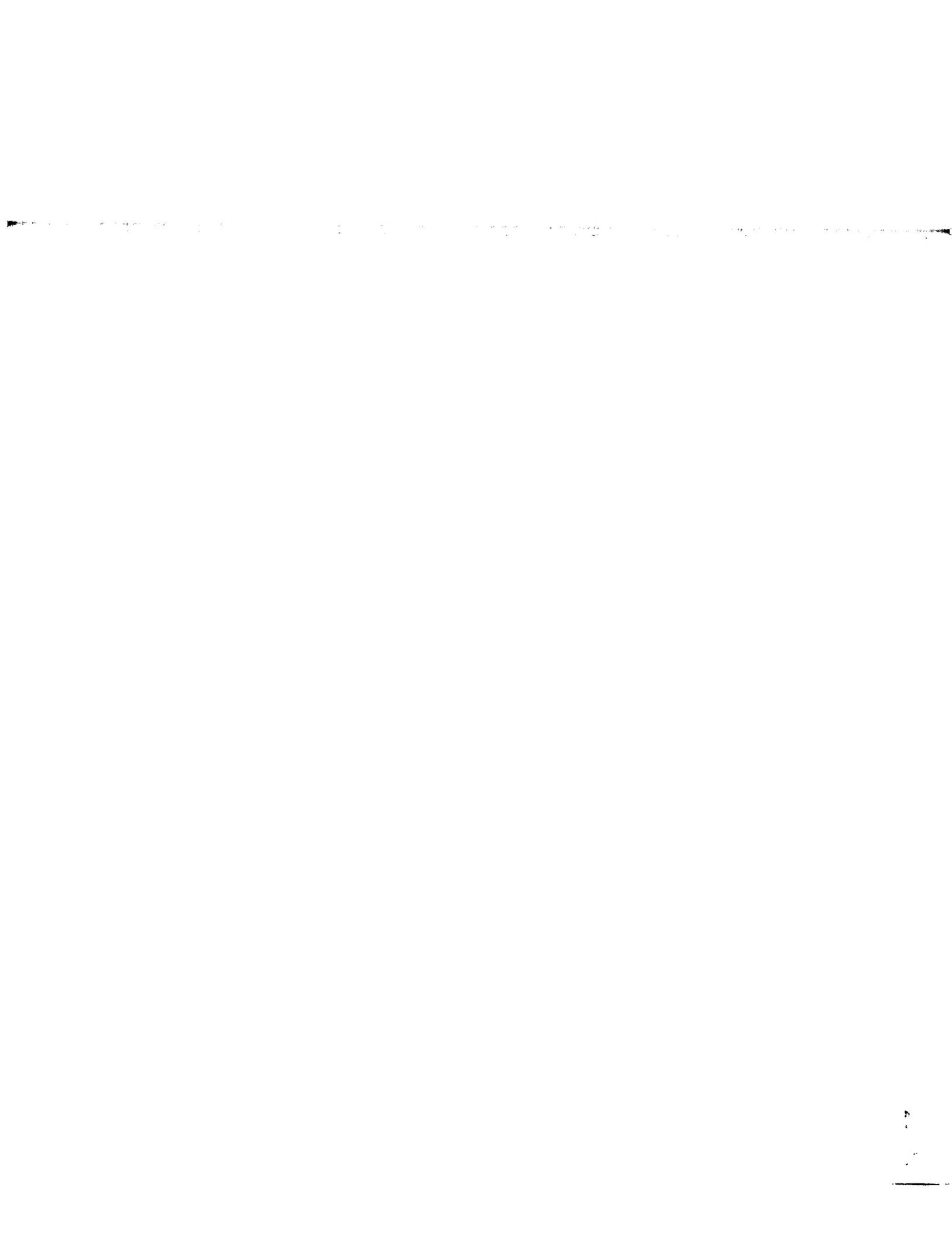
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-19622

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Best Local Similarity 100.0%; Pred. No. 2e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 GPTSS 16
Db 35 GPTSS 39

RESULT 15
US-10-057-498-19622
; Sequence 19622, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Jennifer
; APPLICANT: Skeky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 19622
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-19622

Query Match 26.3%; Score 5; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 GPTSS 16
Db 35 GPTSS 39

Search completed: January 7, 2003, 12:46:01
Job time : 12.2051 secs



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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:38:34 ; Search time 133 Seconds
(without alignments)
92,105 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

Sequence: 1 MDGSGXXXXGGPTSSSEQI 19

Scoring table: OLIGO Gapext 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 45669144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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27: /cgn2_6/pidata/1/paa/US61_COMBO.pep:*

RESULT 1

US-09-876-204-1

; Sequence 1, Application US/09876204

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING REAGENTS AND METHODS

; FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09-876, 204

; CURRENT FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 09/166, 028

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic based on consensus sequence of Homo sapiens, Mus musculus, and Rattus norvegicus

; NAME/KEY: VARIANT

; LOCATION: (61)-(10)

; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;

; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;

; OTHER INFORMATION: Xaa at 10 can be S or G;

; OTHER INFORMATION: US-09-876-204-1

Query Match 73.7% ; Score 14; DB 22; Length 19;

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	14	73.7	19	Sequence 1, Appli
2	9	47.4	20	Sequence 3, Appli
3	9	47.4	20	Sequence 4, Appli
4	9	47.4	20	Sequence 5, Appli
5	9	47.4	70	Sequence 1, Appli
6	9	47.4	70	Sequence 2, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Best Local Similarity 100.0%; Pred. No. 4e-07;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

; FILE REFERENCE: 50013/011001
 ; CURRENT APPLICATION NUMBER: US/09/876,204
 ; PRIORITY NUMBER: 2001-06-06
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 20
 ; TYPE: PRT ; ORGANISM: Rattus norvegicus
 US-09-876-204-5

RESULT 2
 US-09-876-204-3

; Sequence 3, Application US/09876204
 ; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING

; REAGENTS AND METHODS

; FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09/876,204

; CURRENT FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 09/166,028

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 20
 ; TYPE: PRT ; ORGANISM: Homo sapiens
 US-09-876-204-3

1 Query Match 47.4%; Score 9; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
 Db 11 GGPTSSSEQI 19

RESULT 3
 US-09-876-204-4

; Sequence 4, Application US/09876204
 ; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING

; REAGENTS AND METHODS

; FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09/876,204

; CURRENT FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 09/166,028

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: PRT ; ORGANISM: Mus musculus
 US-09-876-204-4

Query Match 47.4%; Score 9; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
 Db 11 GGPTSSSEQI 19

RESULT 4
 US-09-876-204-5

; Sequence 5, Application US/09876204
 ; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING

; REAGENTS AND METHODS

; FILE REFERENCE: 50013/011001
 ; CURRENT APPLICATION NUMBER: US/09/876,204
 ; CURRENT FILING DATE: 2001-06-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 20
 ; TYPE: PRT ; ORGANISM: Mus musculus
 US-09-876-204-5

Query Match 47.4%; Score 9; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
 Db 11 GGPTSSSEQI 19

Db 11 GGPTSSEQI 19 US-09-177-315 1

RESULT 7 PCT-US99-24747-5 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 5, Application PC/TUS9924747 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; CURRENT APPLICATION NUMBER: PCT/US99/24747
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: 6029-1754
 ; CURRENT APPLICATION NUMBER: PCT/US99/24747-5
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FILE REFERENCE: 6029-1754
 ; CURRENT APPLICATION NUMBER: PCT/US99/24747-6
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FILE REFERENCE: 6029-1754-6

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-2

RESULT 8 PCT-US99-24747-6 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 6, Application PC/TUS9924747 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; CURRENT APPLICATION NUMBER: PCT/US99/24747
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: 6029-1754
 ; CURRENT APPLICATION NUMBER: PCT/US99/24747-5
 ; CURRENT FILING DATE: 1999-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: 6029-1754-5

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-3

RESULT 9 US-09-177-315-1 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 1, Application US-09177315 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; FILE REFERENCE: 6029-5756
 ; CURRENT APPLICATION NUMBER: US/09/177-315
 ; CURRENT FILING DATE: 1998-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: 6029-5756

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-6

RESULT 10 US-09-177-315-2 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 2, Application US-09177315 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; FILE REFERENCE: 6029-5756
 ; CURRENT APPLICATION NUMBER: US/09/177-315
 ; CURRENT FILING DATE: 1998-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FILE REFERENCE: 6029-5756

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-5

RESULT 11 US-09-177-315-5 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 5, Application US-09177315 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; FILE REFERENCE: 6029-5756
 ; CURRENT APPLICATION NUMBER: US/09/177-315
 ; CURRENT FILING DATE: 1998-10-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FILE REFERENCE: 6029-5756

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-4

RESULT 12 US-09-177-315-6 Query Match 47.4%; Score 9; DB 15; Length 70;
 Sequence 6, Application US-09177315 Best Local Similarity 100.0%; Pred. No. 0.17;
 ; GENERAL INFORMATION: M. Mismatches 0; Indels 0; Gaps 0;
 ; APPLICANT: Johnson Jr., Eugene M.
 ; APPLICANT: Easton, Rachael M.
 ; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
 ; FILE REFERENCE: 6029-5756

Query Match 47.4%; Score 9; DB 15; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPTSSEQI 19 US-09-177-315-3

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; CURRENT APPLICATION NUMBER: US/09/177,315
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-177-315-6

RESULT 15
PCT-US99-24747-7
; Sequence 7 Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; ATTORNEY: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-24747-7

Query Match 47.4%; Score 9; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 GGPTTSEQI 19
Db 11 GGPTTSEQI 19

RESULT 13
PCT-US99-24747-3
; Sequence 3 Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; ATTORNEY: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-24747-3

Query Match 47.4%; Score 9; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 GGPTTSEQI 19
Db 11 GGPTTSEQI 19

RESULT 14
PCT-US99-24747-4
; Sequence 4 Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; ATTORNEY: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
; PCT-US99-24747-4

Query Match 47.4%; Score 9; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 GGPTTSEQI 19
Db 11 GGPTTSEQI 19

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:39:54 ; Search time 7.30769 Seconds
(without alignments)
49.274 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

Sequence: 1 MDGSGXXXXGGPTTSSEQI 19

Scoring table: OLIGO Gapext 60.0 , Gapext 60.0

Searched: 117078 seqs, 18951520 residues

Word size : 0

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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14: /cgn2_6/podata/1/pubpaas/US60__PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14	73.7	19	10	US-09-876-204-1
2	9	47.4	20	10	US-09-876-204-3
3	9	47.4	20	10	US-09-876-204-4
4	9	47.4	20	10	US-09-876-204-5
5	9	47.4	331	10	US-09-03555-2
6	6	31.6	154	10	US-09-876-889-16
7	8	5	26.3	20	US-09-205-638-281
8	5	26.3	37	10	US-09-205-638-57
9	5	26.3	38	10	US-09-864-761-41553
10	11	5	26.3	49	US-09-864-761-35953
11	12	5	26.3	50	US-09-864-761-38835
12	13	5	26.3	77	US-10-001-835-143
13	14	5	26.3	89	US-09-764-869-948
14	15	5	26.3	116	US-09-764-853-501
15	16	5	26.3	243	US-09-738-626-5718
16	17	5	26.3	253	US-09-764-870-424
17	18	5	26.3	258	US-09-738-626-4896
18	19	5	26.3	275	US-09-054-141-2
19	5	26.3	324	10	US-09-886-055-81

ALIGNMENTS

```
RESULT 1
US-09-876-204-1
; Sequence 1, Application US/09876204
; General Information
; Applicant: Gordon C. Shore et al.
; Title of Invention: BAX-MEDIATED APOPTOSIS MODULATING
; File Reference: 50013/011001
; Current Filing Date: 2001-06-06
; Prior Application Number: 09/166, 028
; Prior Filing Date: 1998-10-05
; Number of SEQ ID Nos: 7
; Software: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; Other Information: Synthetic based on consensus sequence of Homo
; sapiens, Mus musculus, and Rattus norvegicus
; Name/Key: VARIANT
; Location: (6)-(10)
; Other Information: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; Other Information: Xaa at 10 can be S or G;
; US-09-876-204-1
Query Match Best Local Similarity 73.7%; Score 14; DB 10; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSGXXXXGGPTTSSEQI 19
Db 1 MDGSGXXXXGGPTTSSEQI 19

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RESULT 2
US-09-876-204-3
; Sequence 3, Application US/09876204
; Patent No. US20020052316A1

; GENERAL INFORMATION:
; TITLE OF INVENTION: Gordon C. Shore et al. ;
; TITLE OF INVENTION: REAGENTS AND METHODS ;
; FILE REFERENCE: 50013/011.001 ;
; CURRENT APPLICATION NUMBER: US/09/876,204 ;
; CURRENT FILING DATE: 2001-06-06 ;
; PRIOR APPLICATION NUMBER: 09/166,028 ;
; PRIOR FILING DATE: 1998-10-05 ;
; NUMBER OF SEQ ID NOS: 7 ;
; SOFTWARE: FastSEQ for Windows Version 4.0 ;
; SEQ ID NO 3 ;
; LENGTH: 20 ;
; TYPE: PRT ;
; ORGANISM: Homo sapiens
US-09-876-204-3

Query Match 47.4%; Score 9; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 5
US-09-033-525-2
Sequence 2, Application US/09033525
; Sequence 2, Application US/09033525
; Patent No. US200200090374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben Yehuda, Ahmi
; APPLICANT: Azar, Yehudit
; APPLICANT: Aqeilan, Rami
; APPLICANT: Belototsky, Ruth
; APPLICANT: Lorberbaum-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
; TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT ;
; ORGANISM: Homo sapiens
US-09-033-525-2

Query Match 47.4%; Score 9; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 150 GGPTSSSEQI 158

RESULT 6
US-09-876-889-16
Sequence 16, Application US/09876889
; Sequence 16, Application US/09876889
; Patent No. US20020076715A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C3
; CURRENT APPLICATION NUMBER: US/09/876,889
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 154
; TYPE: PRT ;
; ORGANISM: Homo sapien
US-09-876-889-16

Query Match 31.6%; Score 6; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSEQ 18

US-09-876-204-4
Sequence 4, Application US/09876204
; Sequence 4, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011.001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT ;
; ORGANISM: Mus musculus
US-09-876-204-4

Query Match 47.4%; Score 9; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 4
US-09-876-204-5
Sequence 5, Application US/09876204
; Sequence 5, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011.001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20

Db 64 ||||| PTSSEQ 69

RESULT 9
US-09-205-658-281
; Sequence 281, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkin, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 281
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-205-658-281

Query Match 26.3% Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GPTSS 16
Db 3 GPTSS 7

RESULT 8
US-09-205-658-257
; Sequence 257, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkin, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 257
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-205-658-257

Query Match 26.3% Score 5; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 32; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTS 15
Db 2 GGPTS 6

RESULT 9
US-09-864-761-41953
; Sequence 41953, Application US/09864761
; Patent No. US2002004876A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 41953
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC023344.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; US-09-864-761-41953

Query Match 26.3% Score 5; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 33; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSE 17 ; OTHER INFORMATION: EST_HUMAN HIT: BE707262.1, EVALUE 3 .90e+00
 Db 27 PTSSE 31 ; US-09-864-761-35963

RESULT 10

US-09-864-761-35963 ; Sequence 35963, Application US/09864761
 ; Patent No. US200202048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanel, David K.
 ; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT EXPRESSION ANALYSIS BY MICROARRAY

; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO: 35963
 ; LENGTH: 49

; FEATURE:
 ; OTHER INFORMATION: MAP TO AL109942.4
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
 ; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 2.9
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
 ; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2

Qy 12 GPTSS 16 ; RESULT 11
 Db 33 GPTSS 37 ; US-09-864-761-38835
 ; Sequence 38835, Application US/09864761
 ; Patent No. US2002048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CURRENT EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
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 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO: 38835
 ; LENGTH: 50
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AL031588.1
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: Q46378, EVALUAE 4.70e+00
US-09-864-761-38835; SEQ ID NOS: 14

Query Match Score 5; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 GGPTS 15
Db 42 GGRTS 46

RESULT 12
US-10-001-835-143
; Sequence 143, Application US/10001835
; Patent No. US2002016387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 143
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-835-143

Query Match Score 5; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 GPTSS 16
Db 50 GPTSS 54

RESULT 13
US-09-764-869-948
; Sequence 948, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 948
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-948

Query Match Score 5; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 TSSEQ 18
Db 44 PTSSE 48

RESULT 14
US-09-764-853-501
; Sequence 501, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PU06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 501
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-501

Query Match Score 5; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PTSSE 17
Db 96 PTSSE 100

RESULT 15
US-09-738-626-5718
; Sequence 5718, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MITOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO: 5718
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5718

Query Match Score 5; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Jan 7 13:10:43 2003

us-09-876-204-1.rapb

Page 6

Db 3 TSSEQ 7

Search completed: January 7, 2003, 12:46:23
Job time : 8.30769 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:37:29 ; Search time 11.2051 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 19
Sequence: 1 MDGSGXXXXGGPTTSEQI 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs , 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:
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2: /cggn2_6/podata/1/iiaa/5B_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Description
1	14	73.7	Sequence 1, Appli
2	9	47.4	Sequence 3, Appli
3	9	47.4	Sequence 4, Appli
4	9	47.4	Sequence 5, Appli
5	9	47.4	Sequence 21, Appli
6	9	47.4	Sequence 2, Appli
7	9	47.4	Sequence 21, Appli
8	9	47.4	Sequence 3, Appli
9	9	47.4	Sequence 8, Appli
10	9	47.4	Sequence 9, Appli
11	9	47.4	Sequence 2, Appli
12	9	47.4	Sequence 3, Appli
13	9	47.4	Sequence 8, Appli
14	9	47.4	Sequence 9, Appli
15	9	47.4	Sequence 25, Appli
16	9	47.4	Sequence 13, Appli
17	9	47.4	Sequence 2, Appli
18	9	47.4	Sequence 3, Appli
19	9	47.4	Sequence 8, Appli
20	9	47.4	Sequence 9, Appli
21	9	47.4	Sequence 2, Appli
22	9	47.4	Sequence 3, Appli
23	9	47.4	Sequence 8, Appli
24	9	47.4	Sequence 9, Appli
25	9	47.4	Sequence 2, Appli
26	9	47.4	Sequence 3, Appli
27	9	47.4	Sequence 8, Appli

28 9 47.4 192 2 US-08-856-034-9
29 9 47.4 192 4 US-09-127-048-6
30 9 47.4 192 4 US-08-927-326-3
31 9 47.4 192 4 US-08-927-326-8
32 9 47.4 192 4 US-08-927-326-9
33 9 47.4 192 5 PCT-US95-04600-25
34 9 47.4 192 5 PCT-US95-04600-25
35 9 47.4 192 5 PCT-US95-04600-25
36 9 47.4 192 5 PCT-US95-04600-25
37 9 47.4 221 1 US-08-616-732A-9
38 9 47.4 221 4 US-09-037-742B-9
39 6 31.6 120 4 US-09-134-001C-5332
40 6 31.6 154 4 US-09-397-787-16
41 6 31.6 932 4 US-09-071-035-16
42 6 31.6 969 4 US-08-514-975B-2
43 6 31.6 2165 1 US-09-071-035-414
44 5 26.3 2165 5 PCT-US95-1250-2
45 5 26.3 5 1 US-08-798-897-20

ALIGNMENTS

RESULT 1
US-09-166-028-1
; Sequence 1, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/2011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo
; NAME/KEY: VARIANT
; LOCATION: (6..110)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; OTHER INFORMATION: Xaa at 8 can be L or R; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-166-028-1
Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSXXXXGGPTTSF01 19
Db 1 MDGSXXXXGGPTTSF01 19
RESULT 2
US-09-166-028-3
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/2011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 3

;

LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-028-3

Query Match 47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 3
US-09-166-028-4
Sequence 4, Application US/09166028
GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-166-028-4

Query Match 47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 4
US-09-166-028-5
Sequence 5, Application US/09166028
GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-166-028-5

Query Match 47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 5
US-08-798-897-21
Sequence 21, Application US/08798897

;

Patent No. 5789201
GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-798-897-21

Query Match 47.4%; Score 9; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGPTSSSEQI 19
Db 6 CGPTSSSEQI 14

RESULT 6
US-08-798-523-21
Sequence 21, Application US/08978523
GENERAL INFORMATION:
; APPLICANT: Guastella, John
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897
 FILING DATE: February 11, 1997
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 424
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 1483.0140002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-978-523-21

Query Match	47.4%	Score 9;	DB 2;	Length 25;
Best Local Similarity	100.0%	pred. No.	0.0027;	
Matches	9;	Mismatches	0;	Indels 0;
				Gaps 0;

Qy 11 GGPTSSSEQI 19
 Db 6 GGPTSSSEQI 14

RESULT 7
 US-08-112-208C-2
 Sequence 2, Application US/08112208C
 ; Patent No. 5691179
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/112,208C
 ; FILING DATE: 26-AUG-1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15726A-000610
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..192
 ; OTHER INFORMATION: /note= "protein sequence of murine
 ; US-08-112-208C-3

Query Match 47.4%; Score 9; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
 Db 11 GGPTSSSEQI 19

RESULT 9
 US-08-112-208C-8
 Sequence 8, Application US/08112208C
 ; Patent No. 5691179
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:

Query Match 47.4%; Score 9; DB 1; Length 192;
 Best Local Similarity 100.0%; pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
 ;

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-0000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-208C-8

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 10
US-08-112-208C-9
; Sequence 9, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-0000610
; TELEPHONE: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 11
US-08-248-819A-2
; Sequence 2, Application US/08248819A
; Patent No. 570638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/2488,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-0000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSSEQI 19
Db 11 GGPTSSSEQI 19

RESULT 12
US-08-248-819A-3
; Sequence 3, Application US/08248819A
; Patent No. 570638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-0000610
; TELEPHONE: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-208C-9

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COUNTRY: US
 2 LP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248, 819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112, 208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30, 223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 FEATURE:
 NAME/KEY: protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Protein sequence of murine
 OTHER INFORMATION: Box."
 ;US-08-248-819A-3

Query Match Score 9; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 US-08-248-819A-8
 ; Sequence 8, Application US/08248819A
 ; Patent No. 5700638
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/248, 819A
 ; FILING DATE: 25-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/112, 208
 ; FILING DATE: 26-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30, 223
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ;US-08-248-819A-9

Query Match Score 9; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

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 Db 11 GGPTSEQI 19
 QY 11 GGPTSEQI 19
 Db 11 GGPTSEQI 19

RESULT 15
US-08-607-269-25
; Sequence 25, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Kathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-607-269-25

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

Search completed: January 7, 2003, 12:40:51
Job time : 11.2051 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	69	88.5	24	11 Q8VHY7	
2	67	85.9	24	4 Q8WXU1	
3	67	85.9	164	4 Q9QD6	
4	67	85.9	179	4 Q9NYG7	
5	58	74.4	192	6 Q8S043	
6	41	52.6	315	17 QBTIC5	
7	40	52.6	625	5 Q9NE37	
8	40	51.3	487	3 Q05377	
9	40	51.3	492	3 Q12317	
10	40	51.3	528	3 Q05378	
11	40	51.3	893	11 Q99L15	
12	39	50.0	248	16 Q9CG22	
13	39	50.0	677	5 Q9RNJ1	
14	39	50.0	1323	6 Q75509	
15	38	48.7	175	2 Q9WDX4	
16	38	48.7	297	4 Q9BVF5	

OX	NCBI_TaxID=2214;	Qy	4 SGXXXXGGPTSS 16
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN_C2A / ATCC 35395 / DSM 2834;		
RX	MEDLINE=21939760; PubMed=11932238;		
RA	Galagan J.E., Nusbaum C., Roy A., McDonald P.,		
RA	FitzHugh W., Calvo S., Enebo R., Smirnov S., Atnoor D., Brown A.,		
RA	Allison N., McElroy J., Stander-Thomann K., Dearellano K., Johnson R.,		
RA	Linton L., McEwan P., Zimmermann K., Talamas J., Tirrell A., Ye W.,		
RA	Zimmer A., Barber R.D., Cain I., Graham D.E., Grahame D.A., Guss A.M.,		
RA	Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,		
RA	Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,		
RA	Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,		
RA	Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,		
RA	Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Landen E.,		
RA	Metcalf W.W., Birren B.,		
RT	"The genome of Methanobarcina acetivorans reveals extensive metabolic and physiological diversity.";		
RL	Genome Res. 12:522-542(2002).		
DR	EMBL; AR01134; AAC07575.1; -.		
KW	Complete proteome;		
SQ	SEQUENCE 315 AA; 34004 MW; 3649A8CBE8784486 CRC64;		
RESULT 7	Query Match 52.6%; Score 41; DB 17; Length 315;		
Best Local Similarity 57.1%; Pred. No. 9.9;			
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;			
Qy	3 GSGXXXXGGPSS 16		
DB	249 GAGGAGGGPSS 262		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomyces;		
OK	NCBI_TaxID=932;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96076631; PubMed=7502582;		
RA	Vandenbol M., Durand P., Portetelle D., Hilger F.;		
RT	"Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Ty1-H3 retrotransposon, the sufl(+)-frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a delta element.";		
RT	Year 11:1069-1075(1995);		
RL	EMBL; Z48149; CAM88149.1; -.		
DR	SGD; S0005472; MSB4		
DR	InterPro; IPR000195; RadGAP_TBC.		
DR	SMART; SM00164; TBC; 1.		
DR	Pfam; PF00566; TBC; 1.		
SQ	SEQUENCE 487 AA; 56331 MW; B4FCFF5632F771F CRC64;		
RESULT 8	Query Match 51.3%; Score 40; DB 3; Length 487;		
Best Local Similarity 38.9%; Pred. No. 25;			
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;			
Qy	1 MDGSXXXXGGPTSS 18		
DB	310 MNGNGSTQDISPASGE 327		
RESULT 9	Query Match 51.3%; Score 40; DB 3; Length 487;		
ID	Q12317 PRELIMINARY; PRIT; 492 AA.		
AC	Q12317:		
DT	01-NOV-1996 (TREMBREL; 01, Created)		
DT	01-NOV-1996 (TREMBREL; 01, Last sequence update)		
DR	01-JUN-2002 (TREMBREL; 21, Last annotation update)		
DE	Chromosome XI / reading frame ORF YOL112W.		
GN	MSB4 OR YOL112W.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Durand P., Hilger F., Portetelle D., Vandenbol M.;		
RA	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.		
DR	InterPro; IPR000529; DEAD_box.		
DR	InterPro; IPR001650; Helicase_C.		
DR	pfam; PF00270; DEAD; 1.		
DR	pfam; PF00271; helicase_C; 1.		
DR	SMART; SM00487; DEEXDC; 1.		
DR	SMART; SM00490; HELIC; 1.		
DR	PROSITE; PS00039; DEAD_ATP_HELICASE; UNKNOWN_1.		
DR	ATP-binding; Helicase.		
SQ	SEQUENCE 625 AA; 66776 MW; 01D457D7F4FBCB5 CRC64;		
Query Match 52.6%; Score 41; DB 5; Length 625;			
Best Local Similarity 61.5%; Pred. No. 21;			
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			

RL Yeast 11-1069-1075(1995);
DR EMBL; 274854; CAA90131.1; -.
DR SGG; S005472; MSB4.
DR InterPro; IPR00195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1;
SQ SEQUENCE 492 AA; 57092 MW; CB411DBB56003929 CRC64;

Query Match 51.3%; Score 40; DB 3; Length 492;
Best Local Similarity 38.9%; Pred. No. 25; Mismatches 7; Conservative 3; Indels 8; Gaps 0; Gaps 0;
Db 310 MNGNGSTDQISGPASGEE 327

RESULT 10
Q05378 PRELIMINARY; PRT; 528 AA.
ID Q05378; AC 005378;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chromosome XV DNA (44 KB fragment).
GN MSB4 AND YOL112W.

OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetidae; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE:96076631; PubMed=7502582;
RA Vandenberg M., Duind P., Portetelle D., Hilger F.;
RT Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT including the Ty1-R3 retrotransposon, the suf1(+)-frameshift
RT suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
RT delta element.;
RL Yeast 11:1069-1075(1995).
DR EMBL; ZA8149; CAA8150.1; -.
DR SGD; S0005472; MSB4.
DR InterPro; IPR00195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
DR SEQUENCE 528 AA; 61225 MW; 0B65AA34ABER676A CRC64;

Query Match 51.3%; Score 40; DB 3; Length 528;
Best Local Similarity 38.9%; Pred. No. 27; Mismatches 7; Conservative 3; Indels 8; Gaps 0; Gaps 0;
Db 310 MNGNGSTDQISGPASGEE 327

RESULT 11
Q99L15 PRELIMINARY; PRT; 893 AA.
ID Q99L15; AC 099L15;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-MAR-2002 (TREMBLrel. 17, Last sequence update)
DE Similar to zinc finger protein 281.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphati; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003243; AAC03243.1; -.

RESULT 12
Q9CGZ2 PRELIMINARY; PRT; 248 AA.
ID Q9CGZ2; AC 09CGZ2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4).
GN DACB OR LI0950.

OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIL403;
RA MEDLINE:21235186; PubMed=11334741;
RA Boletin A., Wincker P., Mauzer S., Jaillon O., Malarrie K.,
RA Weissenbach J., Ehrlrich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lacticis ssp. Lacticis TIL403.";
RL Genome Res. 11:731-731(2001).
DR EMBL; AE006329; AAC05048.1; -.
MEROPS; M15.050; -.
DR InterPro; IPR003709; VNY.
DR Pfam; PF02557; VNY; 1.
DR Carboxypeptidase; complete proteome.
KW SEQUENCE 248 AA; 27478 MW; E64427D05CF81CC6 CRC64;

Query Match 50.0%; Score 39; DB 16; Length 248;
Best Local Similarity 38.9%; Pred. No. 19; Mismatches 7; Conservative 2; Indels 9; Gaps 0; Gaps 0;
Db 134 MNGGCTVNSSGNPISSEE 151

RESULT 13
Q9NNI1 PRELIMINARY; PRT; 677 AA.
ID Q9NNI1; AC 09NNI1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Possible k0649.1 protein.
GN LM15-1.82.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.

RA STRAIN=FYRIEDIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

RN [2]
 RE SEQUENCE FROM N.A.
 RC
 RX STRAIN="FRIEDLIN";
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
 RT "A physical map of the *Leishmania* major Friedlin genome.";
 DR Genome Res. 8:135-145(1998);
 DR EMBL: AL160371; CAC0019; -;
 SQ SEQUENCE 677 AA; 71562 MW; 4FE7D3D13E56C310 CRC64;

Query Match 50.0%; Score 39; DB 5; Length 677;
 Best Local Similarity 50.0%; Pred. No. 55;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Qy 3 CGGXXXXXGGPSSSEQ 18
 Db 528 GS[GIVLDGGPDAWQ 543

RESULT 14
 077509 PRELIMINARY: PRT; 1323 AA.
 ID 077509 AC
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Submaxillary mucin (Fragment).
 GN BSM2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buteraria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99011416; PubMed=9792811;
 RA Jiang W., Woitach J.T., Gupta D., Bhavanandan V.P.;
 RT "Sequence of a second gene encoding bovine submaxillary mucin:
 implication for mucin heterogeneity and cloning.";
 RL Biochem. Biophys. Res. Commun. 251:550-556(1998).
 DR EMBL: AF019298; ACT:2492.1; -;
 DR Interpro; IPR000359; Cys knot.
 DR Interpro; IPR00107; VWF_C.
 DR Pfam; PF00007; Cys knot; 1.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00214; WWC; 1.
 DR PROSITE; PS01185; CRCK_1; 1.
 DR PROSITE; PS01225; CRCK_2; 1.
 DR PROSITE; PS01208; VWFC; 1.
 FPT NON_TER 1
 SQ SEQUENCE 1323 AA; 133693 MW; D2C71C14968B96A8 CRC64;

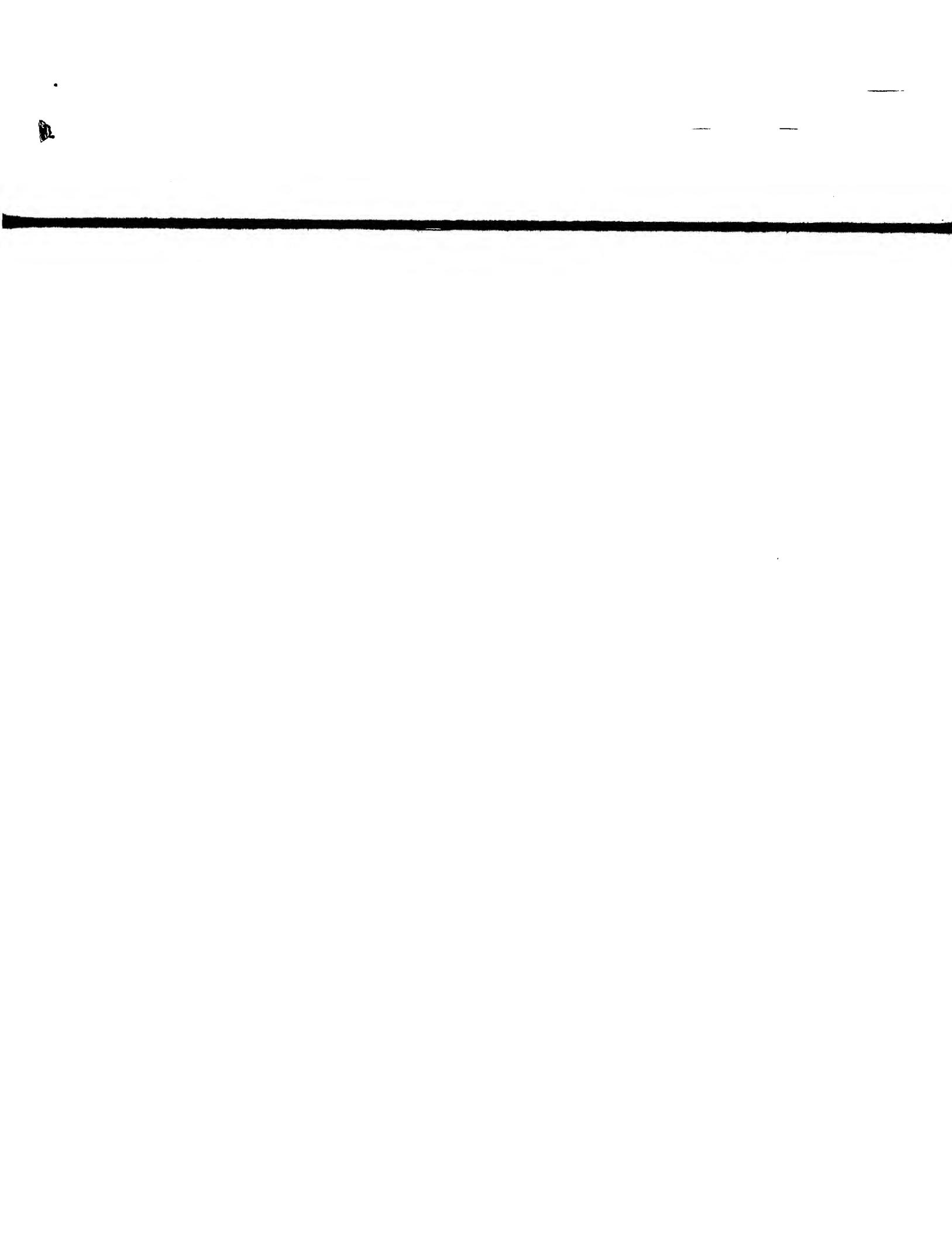
Query Match 50.0%; Score 39; DB 6; Length 1323;
 Best Local Similarity 38.9%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Qy 2 DGS[GIVLDGGPSSQI 19
 Db 271 EGSGTGNGSTAGPTTRI 288

RESULT 15
 09WXD4 PRELIMINARY: PRT; 175 AA.
 ID 09WXD4 AC
 AC 09WXD4; DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE EafA.
 GN OS Erwinia aphidicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Erwinia.
 OX NCBI_TaxID=68334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAM4479;
 RA Harada H., Ishikawa H.;
 RT "Sugar induced 17 kDa surface protein of *Erwinia aphidicola* is homologous to major fimbrial subunit of uropathogenic enterobacteria.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB019396; BAA76622.1; -;
 DR InterPro; IPR00259; Fimbrial.
 DR pfam; PF00419; Fimbrial; 1.
 SQ SEQUENCE 175 AA; 17805 MW; 8AA03577A5B171DB CRC64;

Query Match 48.7%; Score 38; DB 2; Length 175;
 Best Local Similarity 38.9%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 Qy 2 DGS[GIVLDGGPSSQI 19
 Db 117 DGS[GKKEI[EGLGPTTAOTL 134

Search completed: January 7, 2003, 12:30:47
 Job time : 25.8718 secs



Copyright (c) 1993 - 2003	GenCore version 5.1.3	Compugen Ltd.
OM protein - protein search, using SW model		
Run on:	January 7, 2003, 12:25:07 ; Search time 7.69231 Seconds	(without alignments)
Title:	US-09-876-204-3	107.838 Million cell updates/sec
Perfect score:	106	
Sequence:	MDGSQFOPRGGGPISSEQIM	20
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Searched:	112892 seqs, 41476328 residues	
Total number of hits satisfying chosen parameters:	112892	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing:	Minimum Match 0%	
Database :	Swissprot_40; *	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Match Length DB ID
1	106	100.0 143 1 BAXD_HUMAN
2	106	100.0 192 1 BAXA_BOVIN
3	106	100.0 192 1 BAXA_HUMAN
4	106	100.0 218 1 BAXA_RAT
5	89	84.0 192 1 BAXA_MOUSE
6	83	78.3 192 1 BAXC_HUMAN
7	65	41 1 BAXD_HUMAN
8	52	49.1 475 1 MTD2_HUMAN
9	47	44.3 397 1 KPPR_MESCR
10	46.5	43.9 321 1 ISP_BACCR
11	46	43.4 402 1 E1BL_ADEL2
12	46	43.4 654 1 HS70_HYDMA
13	45.5	42.9 434 1 VATB_BORBU
14	45	42.5 351 1 E2BB_HUMAN
15	44.5	42.0 484 1 MEC2_MOUSE
16	44.5	42.0 492 1 MEC2_RAT
17	44	41.5 1241 PER_DROPS
18	44	41.5 1752 1 FLIJ_CAUCR
19	44	41.5 404 1 KPPR_SPTOL
20	44	41.5 511 1 FAST_MOUSE
21	44	41.5 571 1 IF2_THETH
22	44	41.5 1241 PER_DROPS
23	44	41.5 1848 1 CCAER_DROME
24	43	40.6 340 1 ERMA_ARTS3
25	43	40.6 486 1 MECC_HUMAN
26	43	40.6 501 1 IRK3_HUMAN
27	43	40.6 507 1 CP5G_CANTR
28	43	40.6 524 1 CP5G_CANTR
29	42.5	40.1 1752 1 RPBL_SCHPO
30	42.5	40.1 460 1 VATB_METM
31	42.5	40.1 3511 MY1_MOUSE
32	42	39.6 319 1 K6PF_LACDE
33	42	39.6 347 1 UTR2 YEAST
ALIGNMENTS		
Description		
P55269 homo sapien		
P02703 bos taurus		
Q07812 homo sapien		
Q01814 homo sapien		
Q06690 rattus norv		
Q07813 mus musculu		
Q00815 homo sapien		
Q52964 rhizobium m		
P27774 mesembryant		
P22140 bacillus cl		
P01491 human adeno		
Q55944 hydra magni		
Q51120 borrelia bu		
P41770 homo sapien		
Q922df mus musculu		
Q00566 rattus norv		
P02969 caulobacter		
P05559 spinacia ol		
P20302 triticum ae		
Q93ix9 mus musculu		
P48515 thermus the		
P13348 drosophila		
P91645 drosophila		
P0891 arthropbacte		
P51608 homo sapien		
P44549 homo sapien		
P31609 candida tro		
P31608 candida tro		
P35594 schizosacch		
Q6187 methanoscarch		
Q96224 mus musculu		
P8019 lactobacill		
P32623 saccharomy		
QY		
34	42	39.6 440 1 PDA6_CAEEL
35	42	39.6 501 1 IRK3_MOUSE
36	42	39.6 1150 1 APMU_PIG
37	42	39.6 1171 1 DPOL_HSVT2
38	41.5	39.2 1505 1 CUTL_HUMAN
39	41	38.7 147 1 HOLC_ECOLI
40	41	38.7 216 1 VP2_CAV26
41	41	38.7 216 1 VP2_CAV82
42	41	38.7 322 1 K6P1 THETH
43	41	38.7 329 1 K6PF DEIRA
44	41	38.7 476 1 HLX1 MOUSE
45	41	38.7 476 1 HLX1_MOUSE
Q11067 caenorhabdi		
P35562 mus musculu		
P12021 suis scrofa		
O9yus2 herpesvirus		
P39880 homo sapien		
P28005 escherichia		
P54092 chicken ane		
P54093 chicken ane		
Q93151 chicken ane		
P21777 thermus the		
Q9rwml deinococcus		
Q61670 mus musculu		

Db	Best Local Similarity	Pred.	No.	Matches	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
1	MDGSGEQPREGGPISSEQIM	20										
RESULT 2												
BAXA_BOVIN	STANDARD;	PRT;	192 AA.									
ID 002703;												
AC DT 15-JUL-1999 (Rel. 38, last sequence update)												
DT 15-JUN-2002 (Rel. 41, last annotation update)												
DE Apoptosis regulator BAX, membrane isoform alpha.												
BAX.												
GN Bos taurus (Bovine).												
OC Bovidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;												
OC Bovidae; Bovinae; Bos.												
OX NCBI_TaxID=9913;												
RN [1]												
RP SEQUENCE FROM N.A.												
RC STRAIN=Holstein; TISSUE=Thymus;												
RX MEDLINE=98162580; PubMed=9501056;												
RA "Increased ratio of bcl-2/bax expression is associated with bovine leukemia virus-induced leukemogenesis in cattle.";												
RL Virology 242:184-192(1998).												
CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE CESSATION OF SPERM PRODUCTION BY SIMILARITY).												
CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERO DIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).												
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).												
CC -!- ALTERNATIVE PRODUCTS: A 21 kDa membrane protein alpha and the two cytoplasmic proteins beta and gamma are generated by alternative splicing.												
CC -!- DOMAIN: INFLUENT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).												
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BHL) DOMAIN.												
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.												
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.												
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CC EMBL: U92569; AAC48806; 1; -												
DR HSSP; Q0781; 1MAZ.												
DR InterPro; IPR002475; BCL2_FAMILY.												
DR Pfam; PF00452; BCL2; 1.												
DR SMARF; SM00337; BCL; 1.												
DR PROSITE; PS01080; BH1; 1.												
DR PROSITE; PS01258; BH2; 1.												
DR PROSITE; PS01259; BH3; 1.												
DR PROSITE; PS00662; BCL2_FAMILY; 1.												
KW Apoptosis; Transmembrane; Alternative splicing.												
FT DOMAIN 59 73 BH3.												
FT DOMAIN 98 118 BH1.												
FT DOMAIN 150 165 BH2.												
FT TRANSMEM 172 192 POTENTIAL.												
SQ SEQUENCE 192 AA; 21259 MW; 6BAD5BAB1D5F87E CRC64;												
Query Match	100.0%	Score	106	DB	1	Length	192					

Matches 17; **conservative** 0; **Mismatches** 3; **Indels** 0; **Gaps** 0;

RESULT 7

BAXC_HUMAN	STANDARD:	PRT:	41 AA.
ID BAXC_HUMAN			
AC 007815;			
DT 01-FEB-1995 (Rel. 31, Created)			
DT 01-FEB-1995 (Rel. 31, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE BAX protein, cytoplasmic isoform gamma.			
GN BAX.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX TISSUE=B-cell;			
RX MEDLINE=93364978; PubMed=8358790;			
RA Oltrai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.;			
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death.";			
RL Cell 74:609-619(1993).			
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC -!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.			
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			

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RESULT 8

MOTD_RHIME	STANDARD:	PRT:	475 AA.
ID MOTD_RHIME			
AC 032964;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE Chemotaxis motD protein (Motility protein D).			
GN MOTD.			
OS Rhizobium meliloti (Sinorhizobium meliloti);			
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC Rhizobiales; Sinorhizobium.			
OX NCBI_TAXID=382;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=RJ11/001;			

Query Match 61.3%; Score 65; DB 1; Length 41;
Best Local Similarity 72.2%; Pred. No. 0.0046; Mismatches 1; Mismatches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGGPSSSEQ 18

|||||| ||||| :|||

Dy 1 MDGSGEOPRGGGPSSSEQ 18

Query Match 61.3%; Score 65; DB 1; Length 41;
Best Local Similarity 72.2%; Pred. No. 0.0046; Mismatches 1; Mismatches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGGPSSSEQ 18

|||||| ||||| :|||

Dy 1 MDGSGEOPRGGGPSSSEQ 18

RESULT 9

KPPR_MESCR	STANDARD:	PRT:	397 AA.
ID KPPR_MESCR			
AC P27774;			
DT 01-AUG-1992 (Rel. 23, Created)			
DT 01-AUG-1992 (Rel. 23, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19) (Phosphoribulokinase) (PRK).			
DE Mesembryanthemum crystallinum (Common ice plant).			
OS Mesembryanthemum crystallinum (Common ice plant).			
OC Eukaryota; Viridiplantae; Streptophytina; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.			
OX NCBI_TAXID=3144;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Michalowski, C.B.; Derocher, E.J.; Bohnert, H.J.; Salvucci, M.E.;			
RL Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.			
CC -!- CATALYTIC ACTIVITY: ATP + D-ribulose 5 phosphate = ADP + D-			
CC ribulose 1,5-bisphosphate.			
CC -!- ENZYME REGULATION: LIGHT REGULATED VIA THIOREDOXIN BY REVERSIBLE OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.			
CC -!- PATHWAY: Calvin cycle.			
CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.			

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DR EMBL-M3707; AAA33034; -.

DR InterPro; IPR001324; PRK.

DR Pfam; PF0485; PRK; 1.

DR PRINTS; PR00478; PRIBOKINASE.

DR PROSITE; PS0567; PHOSPHORIBULOKINASE; 1.

DR KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle; ATP-binding; Photosynthesis.

RL Eur. J. Biochem. 210:683-691(1992).
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AE001122; AAC66484.1; -.
 DR TIGR: BB0093; -.
 DR InterPro: IPR004100; ATPase_a/bN
 DR InterPro: IPR00194; ATPase,a/bcentre.
 DR Pfam: PF00006; ATP-synt_ab; 1;
 DR Pfam: PF00005; ATP-synt_ab; N; 1
 DR PRODOM: PS00152; ATPase_alpha_beta; FALSE_NEG.
 DR PROSITE: PS00152; ATPASE_ALPHA_BETA; FALSE_NEG.
 DR PROSITE: PS00089; HSP70_1.
 DR PROSITE: PS00329; HSP70_2; 1.
 DR PROSITE: PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SEQUENCE 654 AA; 71467 MW; SBC1EA4BALE640FB CRC64;
 Query Match 43.4%; Score 46; DB 1; Length 654;
 Best Local Similarity 52.9%; Pred. No. 36;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MGSGSKASSGGPPTIE 652
 DB 636 MGSGSKASSGGPPTIE 652
 RESULT 13
 VATB_BORBU STANDARD: PRIT; 434 AA.
 AC 051120;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit;
 DE ATPB OR BB0093.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TAXID:139;
 RP STRAIN=ATCC 35210 / B31;
 RK MEDLINE=98305943; PubMed=9403685;
 RA Fraser C.M., Castens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Wathey L., McDonald L., Arriach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Ventler J.C.;
 RT "Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*";
 RL Nature 390:580-586(1997).
 CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE V-TYPE BETA CHAIN IS A
 CC REGULATORY SUBUNIT.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + Phosphate +
 CC H(+) (Out).
 CC -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AE001122; AAC66484.1; -.
 DR TIGR: BB0093; -.
 DR InterPro: IPR004100; ATPase_a/bN
 DR InterPro: IPR00194; ATPase,a/bcentre.
 DR Pfam: PF00006; ATP-synt_ab; 1;
 DR Pfam: PF00005; ATP-synt_ab; N; 1
 DR PRODOM: PS00152; ATPase_alpha_beta; FALSE_NEG.
 DR PROSITE: PS00152; ATPASE_ALPHA_BETA; FALSE_NEG.
 DR PROSITE: PS00089; HSP70_1.
 DR PROSITE: PS00329; HSP70_2; 1.
 DR PROSITE: PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SEQUENCE 434 AA; 48026 MW; 5PF023DBD91361B CRC44;
 Query Match 42.9%; Score 45.5; DB 1; Length 434;
 Best Local Similarity 47.4%; Pred. No. 28;
 Matches 9; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 QY 2 DGSGEQPQQGPPSSEQIM 20
 DB 88 DGSG-NPRDGPGPSLDDNNI 105
 RESULT 14
 E2BB_HUMAN STANDARD: PRIT; 351 AA.
 ID E2BB_HUMAN
 AC P43770; 043201;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Translation initiation factor eIF-2B beta subunit (eIF-2B GDP-GTP
 DE exchange factor) (S201115) (S2011115).
 GN EIF2B2 OR EIF2BB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=brain.
 RA Yu W., Sarginson J., Gibbs R.A.;
 RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95319502; PubMed=7596406;
 RA Shirinaton R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
 RA Ikeda M., Choi H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
 RA Focin J., Bruni A.C., Montes M.P., Sorbi S., Rainero I.,
 RA Pinesi L., Nee L., Chumakov I., Pollen D., Brookes A.,
 RA Saucan P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines J.L.,
 RA Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
 RA Rommens J.M., St George-Hyslop P.H.;
 RA "Cloning of a gene bearing missense mutations in early-onset familial
 RT Alzheimer's disease.";
 RL Nature 375:754-760(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Roven L., Madan A., Qin S., Abbasi N., Dors M., Dickhoff R., James R.,
 RA Loetze C., Lasky S., Madan A., Prescott S., Ratcliffe A., Shaffer T.,
 RA Hood L.;
 RT "Sequencing of human chromosome 14.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.
 RN [4]
 RP VARIANTS VWM GLY-213; ARG-273; ASP-316 AND VAL-329.
 RX MEDLINE=21583742; PubMed=11704758;
 RA Leeuw G., Vermeulen G., Koest A.A.M., Naidu S., Mulders J.,
 RA Visser A., Kersbergen P., Mobach D., Fonds D., van Berkel C.G.M.,
 RA Lemmers R.J.H.F., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,
 RA Pronk J.C., van der Kraaij M.S.;
 RT "Subunits of the translation initiation factor eIF2B are mutant in
 RT leukoencephalopathy with vanishing white matter.";
 RL Gemel, 22:383-389(2001).
 CC -!- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR



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Gencore version 5.1.3

OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:08 ; Search time 13.8462 Seconds
 (without alignments)
 138.861 Million cell updates/sec

Title: US-09-876-204-3
 Perfect score: 106
 Sequence: 1 MDGSSEQPRGGPSSSEQIM 20

Scoring table: BLOSUM2
 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	106	100.0	143	bcl-2-associated p	RESULT 1
2	106	100.0	179	Bax delta protein	I38921
3	106	100.0	192	bcl-2-associated p	N;Alternate names: BAX; programmed cell death membrane protein x delta
4	106	100.0	218	bcl-2-associated p	C;Species: Homo sapiens (man)
5	83	78.3	192	d47538	C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000
6	65	61.3	41	C47538	C;Accession: I38921
7	54	50.9	302	S71334	R;Apte, S.S.; Mattei, M.G.; Olsen, B.R.
8	50	47.2	743	T47849	Genomics 26, 592-594, 1995
9	49	46.2	513	D98225	A;Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of
10	49	46.2	513	AC1061	A;Reference number: I38921; MUID:95331797; PMID:6707685
11	49	46.2	1191	T13850	A;Accession: I38921
12	48	45.3	137	G72666	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
13	47.5	44.8	531	T08766	A;Molecule type: mRNA
14	47	44.3	397	T12436	A;Residues: -1-43 <RES>
15	46.5	43.9	321	1 S27501	A;Cross-references: EMBL:U19599; NID:9841237; PIDN: AAC50142.1; PID:9841238
16	46	43.4	482	ERAD24	A;Gene: GDB:BAX
17	46	43.4	524	A69081	A;Map position: 19q13.3-19q13.4
18	46	43.4	627	T18772	A;Cross-references: GDB:228082; OMIM:600040
19	46	43.4	654	S27004	A;Superfamily: bcl transforming protein
20	45.5	42.9	434	E70111	ALIGMENTS
21	45	42.5	397	T30168	Query Match 100.0%; Score 106; DB 2; Length 143;
22	45	42.5	672	I40333	Best Local Similarity 100.0%; Pred. No. 3.3e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23	45	42.5	1284	T13168	Db 1 MDGSSEQPRGGPSSSEQIM 20
24	44.5	42.0	492	A41907	RESULT 2
25	44.5	42.0	22318		JC255
26	44	41.5	247	H87703	Bax-delta protein - human
27	44	41.5	276	1 FLO12C	C;Species: Homo sapiens (man)
28	44	41.5	352	T05643	C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
29	44	41.5	402	2 S02099	C;Accession: JC7255
					A;Molecule type: mRNA
					A;Residues: 1-179 <SCH>
					A;Cross-references: GB:AF247393
					A;Experimental source: cancer promyelocytic cells
					C;Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It activates caspase-3.
					C;Superfamily: bcl transforming protein
					C;Keywords: transmembrane protein

Best Local Similarity 100.0%; Pred. No. 4.1e-08; Mismatches 0; Indels 0; Gaps 0; Result 3

Query 1 MDSGEQPREGGTSSQIM 20
Db 1 MDSGEQPREGGTSSQIM 20

C;Species: Homo sapiens (man)
N;Alternate names: BAX; programmed cell death membrane protein x alpha
C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A;Reference number: A47538; MUID:93364978; PMID:8358790
A;Accession: A47538
A;Molecule type: mRNA
A;Cross-references: GB:L22473; NID:9388165; PIDN:AAA03619.1; PID:9388166
A;Note: the amino end of the mature protein is blocked

C;Genetics:
A;Gene: BAX
A;Gen: BAX
A;Cross-references: GDB:228082; OMIM:600040

C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembrane domain; transmembrane #status predicted <TMH>

Query Match 100.0%; Score 106; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.1e-08; Mismatches 0; Indels 0; Gaps 0; Result 4

Query 1 MDSGEQPREGGTSSQIM 20
Db 1 MDSGEQPREGGTSSQIM 20

N;Alternate names: BAX; programmed cell death membrane protein x beta
C;Species: Homo sapiens (man)
C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Accession: B47538
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A;Reference number: A47538; MUID:93364978; PMID:8358790
A;Accession: A47538
A;Molecule type: mRNA
A;Cross-references: GB:L22473; NID:9388165; PIDN:AAA03621.1; PID:9388166
A;Note: the amino end of the mature protein is blocked

C;Genetics:
A;Gene: BAX
A;Cross-references: GDB:228082; OMIM:600040
A;Map position: 19q13.3-19q13.4
C;Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 61.3%; Score 65; DB 2; Length 41;
Best Local Similarity 72.2%; Pred. No. 0.0074; Mismatches 4; Indels 0; Gaps 0; Result 5

Query 1 MDSGEQPREGGTSSQIM 18
Db 1 MDSGEQPREGGTSSQIM 18

N;Alternate names: BAX; programmed cell death membrane protein x gamma
C;Species: Mus musculus (house mouse)
C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A;Reference number: A47538; MUID:93364978; PMID:8358790
A;Accession: D47538
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <OLT>
A;Cross-references: GB:L22472
C;Genetics:
A;Gene: bax
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; blocked amino end; heterodimer; homodimer

Query Match 78.3%; Score 83; DB 2; Length 192;
Best Local Similarity 85.0%; Pred. No. 9.1e-05; Mismatches 3; Indels 0; Gaps 0; Result 6

Query 1 MDSGEQPREGGTSSQIM 20
Db 1 MDSGEQPREGGTSSQIM 20

C;Species: Homo sapiens (man)
C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
A;Reference number: A47538; MUID:93364978; PMID:8358790
A;Accession: A47538
A;Molecule type: mRNA
A;Cross-references: GB:L22475; NID:9388169; PIDN:AAA03621.1; PID:9388170
A;Note: the amino end of the mature protein is blocked

C;Genetics:
A;Gene: BAX
A;Cross-references: GDB:228082; OMIM:600040
A;Map position: 19q13.3-19q13.4
C;Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 61.3%; Score 65; DB 2; Length 41;
Best Local Similarity 72.2%; Pred. No. 0.0074; Mismatches 4; Indels 0; Gaps 0; Result 7

Query 1 MDSGEQPREGGTSSQIM 18
Db 1 MDSGEQPREGGTSSQIM 18

C;Species: Trichoderma reesei
C;Accession: S71334
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
R;Margolles-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.
Eur. J. Biochem. 237, 553-560, 1996
A;Title: Acetyl xylan esterase from Trichoderma reesei contains an active-site serine
A;Reference number: S71334; MUID:96235218; PMID:8647098
A;Accession: S71334
A;Status: preliminary
A;Molecule type: mRNA

A;Cross-references: EMBL:269256; NID:91431619; PID:e220701; PID:91431620 C;Genetics:
A;Gene: axel
A;Superfamily: fungal cellulose-binding domain homology
F1-20/Domain: signal sequence #status predicted <SG>
F;21-302/Product: acetyl xylan esterase #status predicted <MAT>
F;271-302/Domain: fungal cellulose-binding domain homology <FCB>
Query Match 50.9%; Score 54; DB 2; Length 302; Best Local Similarity 50.0%; Pred. No. 2.2.; Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 1 MDSGEGOPRGGPTSSE 18 Db 237 LSSGGSQPPGGPTTSR 254
RESULT 8 T47849 hypothetical protein T8B10_40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T47849 R;Rieder, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, A.;Rieder, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, A.;Submitted to the Protein Sequence Database, March 2000 A;Reference number: 224478 A;Accession: T47849 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-743 <RIE> A;Cross-references: EMBL:AL138346 A;Experimental source: cultivar Columbia; BAC clone T8B10 C;Genetics: A;Map position: 3 A;Note: T8B10_40
RESULT 9 D98225 hypothetical protein AGR_L_1495 [imported] - Agrobacterium tumefaciens (strain C58, Cerebriforme) #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: D98225 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollman, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58 A;Reference number: A97359; PMID:11743194 A;Accession: D98225 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-513 <KUR> A;Cross-references: GB:AE007870; PIDN:AAK89326_1; PID:915159166; GSPDB:GN00170 C;Genetics: A;Cross-references: GB:AE007870; PIDN:AAK89326_1; PID:915159166; GSPDB:GN00170 A;Map position: linear chromosome
Query Match 47.2%; Score 50; DB 2; Length 743; Best Local Similarity 100.0%; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;
OY 4 SGEQPRGG 12 Db 725 SGEPQRGG 733
RESULT 10 AC3061 hypothetical protein Atu4105 [imported] - Agrobacterium tumefaciens (strain C58, Duplex) #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AC3061 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wober, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; MCClelland, P.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kressan, W.; Perry, M.; Gordon-Kamm, E.W.; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; PMID:11743193 A;Accession: AC3061 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-513 <KUR> A;Cross-references: GB:AE008689; PIDN:AAI44905_1; PID:917742557; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics: A;Gene: Atu4105 A;Map position: linear chromosome
Query Match 45.2%; Score 49; DB 2; Length 513; Best Local Similarity 56.2%; Pred. No. 20; Mismatches 9; Conservative 2; Indels 5; Gaps 0;
OY 3 GSSEQQPRGGGPTSSEQ 18 Db 444 GSEFPPRGGGPFSEDE 459
RESULT 11 T13850 gene u-shaped protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000 C;Accession: T13850 R;Haenlin, M. Submitted to the EMBL Data Library, April 1997 A;Reference number: 217795 A;Accession: T13850 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Cross-references: EMBL:Y12322; NID:e1169964; PID:e1169965; PIDN:CAA72991_1 A;Residues: 1-1191 <HAE> A;Gene: u-shaped A;Cross-references: FlyBase:FBgn0003963 C;Function: C;Description: acts as a transregulator of achaete and scute in the dorsal region of C;Keywords: zinc finger
Query Match 46.2%; Score 49; DB 2; Length 1191; Best Local Similarity 50.0%; Pred. No. 46; Mismatches 11; Conservative 3; Indels 4; Gaps 1;
OY 3 GSG---EQPRGGGPTTSBOIM 20 Db 578 GTGRENVETPRGGGSVTPEQIV 599
RESULT 12 G72666 hypothetical protein APE0758 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000 C;Accession: G72666 R;Rawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamini, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J. Taawa, H.; Takamini, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
OY 3 GSGEQPRGGGPTSSEO 18 Db 444 GSETPPRGGGPESEDE 459

DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72665
A;Status: preliminary
A;Residues: 1-137 <KAW>
A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79735.1; PID:di043521; PID:9510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0758
C;Superfamily: Aeropyrum pernix hypothetical protein APE0758
Query Match 45.3%; Score 48; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 DGSGEQPREGGRSS 16
Db 80 DGLHSQPRGGGSSS 94

RESULT 13
T08760
hypothetical protein DKFZp586M1019.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08760
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08760
A;Molecule type: mRNA
A;Residues: 1-531 <WAM>
A;Cross-references: EMBL:AL050284
A;Experimental source: adult uterus; clone DKFZp586M1019
C;Genetics:
A;Note: DKFZp586M1019.1

Query Match 44.8%; Score 47.5; DB 2; Length 531;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 2 DGS-GEQPRGG 12
Db 113 EGSPGEQPRGG 124

RESULT 14
T12436
phosphoribulokinase (EC 2.7.1.19) - common ice plant
C;Species: *Mesembryanthemum crystallinum* (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Sep-1999
C;Accession: T12436
R;Michalowski, C.B.; DeRoche, E.J.; Bohnert, H.J.; Salvucci, M.E.
submitted to the EMBL Data Library, July 1991
A;Description: Phosphoribulokinase from ice plant: transcription, transcripts and protein
A;Reference number: Z17516
A;Accession: T12436
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-397 <MIC>
A;Cross-references: EMBL:M73707; NID:9167265; PID:9167266
C;Superfamily: phosphoribulokinase
C;Keywords: ATP; Calvin cycle; phosphotransferase

Query Match 44.3%; Score 47; DB 2; Length 397;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GSGGPPRGCGPTSEQI 19
Db 77 GAEGEPGPGGNPDNSNLL 93

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:23 ; Search time 11.7949 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: US-09-876-204-3
Perfect score: 106
Sequence: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Parents_AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/pctus.COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	106	100.0	20	4 US-09-166-028-3
2	106	100.0	192	1 US-08-112-208C-2
3	106	100.0	192	1 US-08-112-208C-9
4	106	100.0	192	1 US-08-248-819A-2
5	106	100.0	192	1 US-08-248-819A-9
6	106	100.0	192	1 US-08-607-269-25
7	106	100.0	192	1 US-08-471-058-13
8	106	100.0	192	2 US-08-37-646A-2
9	106	100.0	192	2 US-08-337-646A-9
10	106	100.0	192	2 US-08-856-531-2
11	106	100.0	192	2 US-08-856-531-9
12	106	100.0	192	2 US-08-856-034-2
13	106	100.0	192	2 US-08-856-034-9
14	106	100.0	192	3 US-08-471-057-13
15	106	100.0	192	4 US-08-127-048-7
16	106	100.0	192	4 US-08-927-326-2
17	106	100.0	192	4 US-08-927-326-9
18	106	100.0	192	5 PCT-US95-04600-25
19	106	100.0	221	1 US-08-616-732A-9
20	106	100.0	221	4 US-09-637-742B-9
21	83	78.3	20	4 US-09-166-028-4
22	83	78.3	192	1 US-08-112-208C-3
23	83	78.3	192	1 US-08-112-208C-8
24	83	78.3	192	1 US-08-248-819A-3
25	83	78.3	192	1 US-08-248-819A-8
26	83	78.3	192	2 US-08-337-646A-3
27	83	78.3	192	2 US-08-337-646A-8

ALIGNMENTS

RESULT 1
US-09-166-028-3
; Sequence 3, Application US/09166028
; Patent No. 624585
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 500113/011001
; CURRENT APPLICATION NUMBER: US-09-166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-166-028-3

Query Match Best local Similarity 100.0%; Score 106; DB 4; Length 20;
Matches 20; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;

OY	1 MDGSGEOPRGGGPNSSEQIM 20
Db	1 MDGSGEOPRGGGPNSSEQIM 20

RESULT 2
US-08-112-208C-2
; Sequence 2, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112-208C

FILING DATE: 26-AUG-1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30-223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-112-208C-2

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-08-112-208C-9
 Sequence 9, Application US/08112208C
 Patent No. 5691179
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248 819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112, 208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30-223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-248-819A-2

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-08-248-819A-2
 Sequence 2, Application US/08248819A
 Patent No. 570638
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

RESULT 5
 US-08-248-819A-9
 Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1
 US-08-112-208C-20
 Sequence 1, Application US/08112208C
 Patent No. 5691179
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30-223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-248-819A-9

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSSEQPRGGGPTSSEQIM 20
 Db 1 MDGSSEQPRGGGPTSSEQIM 20

RESULT 6
 US-08-607-269-25
 ; Sequence 25, Application US/08607269
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; PATENT NO. 5702897
 ; TITLE OF INVENTION: Interaction of Proteins Involved in a
 ; TITLE OF INVENTION: Cell Death Pathway
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,058
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/320,157
 ; FILING DATE: 07-OCT-1994
 ; APPLICATION NUMBER: 08/160,067
 ; FILING DATE: 30-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lehnhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20007.12
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-813-6600
 ; TELEFAX: 415-494-0792
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-471-058-13

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSSEQPRGGGPTSSEQIM 20
 Db 1 MDGSSEQPRGGGPTSSEQIM 20

RESULT 7
 US-08-471-058-13
 ; Sequence 13, Application US/08471058
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieffer, Michael C.
 ; APPLICANT: Barr, Philip J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
 ; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018

Query Match 100.0%; Score 106; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSSEQPRGGGPTSSEQIM 20
 Db 1 MDGSSEQPRGGGPTSSEQIM 20

RESULT 8
 US-08-337-646A-2
 ; Sequence 2, Application US/08337646A
 ; PATENT NO. 5856171
 ; GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/337,646A
 FILING DATE: 10-NOV-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,819
 PRIOR APPLICATION DATA:
 FILING DATE: 25-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000620
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-337-646A-2

RESULT 9
 US-08-337-646A-9
 ; sequence 9, Application US/08337646A
 ; Patent No. 5856171
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 78
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/856,531
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, Donald R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5588
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Human BAX polypeptide"

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,819
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000620
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-337-646A-9

RESULT 10
 US-08-856-531-2
 ; sequence 2, Application US/08856531
 ; Patent No. 5942490
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howell & Haferkamp, L.C.
 ; STREET: 7733 Forsyth Blvd., Suite 1400
 ; CITY: St. Louis
 ; STATE: MO
 ; COUNTRY: USA
 ; ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/856,531
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, Donald R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5588
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-531-2

ADDRESSEE: Howell & Haferkamp L.C.
 STREET: 7133 Forsyth Blvd., Suite 1400
 CITY: St. Louis
 STATE: MO USA

Query Match 100.0%; Score 106; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1 8e-08; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGPTTSEQIM 20
 Db 1 MDGSGEOPRGGPTTSEQIM 20

RESULT 11

US-08-856-531-9
 Sequence 9, Application US/08856531
 Patent No. 5942490

GENERAL INFORMATION:
 APPLICANT: KORSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howell & Haferkamp, L.C.
 STREET: 7133 Forsyth Blvd., Suite 1400
 CITY: St. Louis
 STATE: MO USA

CITY: St. Louis
 STATE: MO USA

COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856, 034

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188

TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION:

/note= "Human BAX polypeptide"

US-08-856-034-2

Query Match 100.0%; Score 106; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1 8e-08; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGPTTSEQIM 20
 Db 1 MDGSGEOPRGGPTTSEQIM 20

RESULT 13

US-08-856-034-9
 Sequence 9, Application US/08856034

Patent No. 5955595

GENERAL INFORMATION:

APPLICANT: KORSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31

COURRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.
 STREET: 7133 Forsyth Blvd., Suite 1400
 CITY: St. Louis
 STATE: MO USACOUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856, 034

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188

TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION:

/note= "Human BAX polypeptide"

US-08-856-531-9

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

RESULT 12

US-08-856-034-2

SEQUENCE 2, Application US/08856034
 Patent No. 5955595

GENERAL INFORMATION:
 APPLICANT: KORSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 106; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1 8e-08; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGPTTSEQIM 20
 Db 1 MDGSGEOPRGGPTTSEQIM 20

TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Human Bax polypeptide"
 ; US-08-856-034-9
 ;
 Query Match 100.0%; Score 106; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; ID NO: 9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDGSGEQPRGGGTSSSEQIM 20
 Db 1 MDGSGEQPRGGGTSSSEQIM 20
 ;
 RESULT 14
 US-08-471-057-13
 ; Sequence 13, Application US/08471057
 ; PATENT NO. 6016887
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ;
 ; APPLICANT: BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FORTER
 ; STREET: 755 Pace Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ;
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,057
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/320,157
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20007.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-08-471-057-13
 ;
 Query Match 100.0%; Score 106; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; ID NO: 9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 US-09-127-048-7
 ; Sequence 7, Application US/09127048
 ; PATENT NO. 6165732
 ; GENERAL INFORMATION:
 ; APPLICANT: Korsmeyer, Stanley J.
 ; TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
 ; FILE REFERENCE: 6029-6052
 ; CURRENT APPLICATION NUMBER: US/09/127,048
 ; EARLIER APPLICATION NUMBER: 60/061,823
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 7
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-127-048-7
 ;
 Query Match 100.0%; Score 106; DB 4; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; ID NO: 9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDGSGEQPRGGGTSSSEQIM 20
 Db 1 MDGSGEQPRGGGTSSSEQIM 20
 ;
 Search completed: January 7, 2003, 12:31:49
 Job time : 11.7949 secs

				Gencore version 5.1.3
Copyright (c) 1993 - 2003	CompuGen Ltd.			
Run on:	January 7, 2003, 12:31:28	Search time	30.2051	Seconds
Scoring table:	OLIGO	(without alignments)		
Score:	83.819	Million cell updates/sec		
Title:	US-09-876-204-1			
Perfect score:	19			
Sequence:	1 MDGSGXXXXGGPSSSEQI 19			
Word size :	0			
Total number of hits satisfying chosen parameters:	908470			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing: Listing first 45 summaries				
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2:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1981.DAT:*			
3:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1982.DAT:*			
4:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1983.DAT:*			
5:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1984.DAT:*			
6:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1985.DAT:*			
7:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1986.DAT:*			
8:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1987.DAT:*			
9:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1988.DAT:*			
10:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1989.DAT:*			
11:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1990.DAT:*			
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21:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA2001.DAT:*			
22:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT:*			
23:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
Result No.	Score	Query Match Length DB ID	Description	SUMMARIES
1	14	73 7 19 21 AAY90735	Apoptotic regulati	RESULT 1 ID AAY90735 standard; peptide: 19 AA.
2	9	4 4 20 21 AAY90736	Human BAX amino ac	XX AC AAY90735;
3	9	4 4 20 21 AAY90737	Mouse BAX amino ac	XX DT 17-AUG-2000 (first entry)
4	9	4 4 20 21 AAY90738	Rat BAX amino acid	XX DE Apoptotic regulation of targeting domain consensus sequence SEQ ID NO:1.
5	9	4 4 20 21 AAY70815	Human neuroprotect	XX FT Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
6	9	47 4 70 21 AAY70817	Mouse neuroprotect	KW Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
7	9	47 4 70 21 AAV70820	Human neuroprotect	KW cell death; cancer; cytostatic.
8	9	47 4 70 21 AAV70821	Mouse neuroprotect	XX OS Homo sapiens.
9	9	47 4 78 21 AAV70818	OS Mus musculus.	OS Rattus norvegicus.
10	9	47 4 78 21 AAV70819	OS	OS
			FH Key Location/Qualifiers	ALIGMENTS
			FT Misc-difference 6 /label= Glu, ASP	
			FT Misc-difference 7 /label= Gln, His	
			FT Misc-difference 8 /label= Leu, Pro	
			FT Misc-difference 9 /label= Arg, GLY	
			FT Misc-difference 10 /label= Ser, GLY	
			FT WO200020446-A2.	
			PN	
			PD 13-APR-2000.	
			XX	

PF 05-OCT-1999; 99MO-IB01680.
 XX
 PR 05-OCT-1998; 98US-0166028.
 XX
 PA (UVMC-) UNIV MCGILL.
 XX

PI Shore GC, Goping S;

XX DR WPI: 2000-303740/26.

PT BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer -
 XX Disclosure; Page 6; 53pp; English.
 CC The present invention describes a pure protein (P1) comprising a BAX polypeptide lacking an apoptotic regulation of targeting (ART) domain. P1 has cytostatic activity and can be used in the modulation of apoptosis. The polypeptides and methods from the present invention are useful for identifying compounds that modulate apoptosis which can then be used for treating cancer. The present sequence represents a consensus sequence for an ART domain derived from human, mouse and rat, which is given in the exemplification of the present invention.

Sequence 19 AA:

Query Match 73.7%; Score 14; DB 21; Length 19;
 CC Best Local Similarity 100.0%; Pred. No. 3.7e-07;
 CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 MDGSGXXXGGPSSSEQI 19
 Db 1 MDGSGXXXGGPSSSEQI 19

RESULT 2

AAV90736 ID AAV90736 standard; peptide; 20 AA.
 XX AC AAV90736;
 XX DT 17-AUG-2000 (first entry)

DE Human BAX amino acid sequence 1 to 20 SEQ ID NO:2.
 XX DE XX APOPTOTIC REGULATION OF TARGETING DOMAIN; ART DOMAIN; BAX; apoptosis;
 KW XX Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
 KW cell death; cancer; cytostatic.
 XX OS Mus musculus.
 XX PN WO200020446-A2.
 XX PD 13-APR-2000.
 XX PT 05-OCT-1999; 99MO-IB01680.
 XX PR 05-OCT-1998; 98US-0166028.
 XX PA (UVMC-) UNIV MCGILL.
 XX PI Shore GC, Goping S;
 XX DR WPI: 2000-303740/26.

PT BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer -
 XX Homo sapiens.
 XX WO200020446-A2.
 XX PD 13-APR-2000.
 XX PR 05-OCT-1999; 99MO-IB01680.
 XX PR 05-OCT-1998; 98US-0166028.
 XX PA (UVMC-) UNIV MCGILL.
 XX PT Shore GC, Goping S;
 XX DR WPI: 2000-303740/26.
 XX PS Example 2; Page 53; 53pp; English.

CC The present invention describes a pure protein (P1) comprising a BAX polypeptide lacking an apoptotic regulation of targeting (ART) domain. P1 has cytostatic activity and can be used in the modulation of apoptosis. The polypeptides and methods from the present invention are useful for identifying compounds that modulate apoptosis which can then be used for treating cancer. The present sequence represents a mouse BAX peptide sequence of amino acids 1 to 20, which is used in an example from the present invention.

SQ Sequence 20 AA;

Query Match 47.4%; Score 9; DB 21; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 0.027;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC The present invention describes a pure protein (P1) comprising a BAX polypeptide lacking an apoptotic regulation of targeting (ART) domain. P1 has cytostatic activity and can be used in the modulation of apoptosis. The polypeptides and methods from the present invention are useful for identifying compounds that modulate apoptosis which can then be used for treating cancer -
 XX Example 2; Page 52; 53pp; English.

useful for identifying compounds that modulate apoptosis which can then be used for treating cancer. The present sequence represents a human BAX peptide sequence of amino acids 1 to 20, which is used in an example from the present invention.

CC Sequence 20 AA;

Query Match 47.4%; Score 9; DB 21; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 0.027;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPPSSSEQI 19
 Db 11 GGPPSSSEQI 19

RESULT 3
 AAY90737 ID AAY90737 standard; peptide; 20 AA.
 XX AC AAY90737;
 XX DT 17-AUG-2000 (first entry)

DE Mouse BAX amino acid sequence 1 to 20 SEQ ID NO:3.
 XX DE XX APOPTOTIC REGULATION OF TARGETING DOMAIN; ART DOMAIN; BAX; apoptosis;
 KW XX cell death; cancer; cytostatic.
 OS Mus musculus.
 XX PN WO200020446-A2.
 XX PD 13-APR-2000.
 XX PT 05-OCT-1999; 99MO-IB01680.
 XX PR 05-OCT-1998; 98US-0166028.
 XX PA (UVMC-) UNIV MCGILL.
 XX PI Shore GC, Goping S;
 XX DR WPI: 2000-303740/26.

PT BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer -
 XX Disclosure; Page 6; 53pp; English.
 XX DR WPI: 2000-303740/26.
 XX PS Example 2; Page 52; 53pp; English.

CC The present invention describes a pure protein (P1) comprising a BAX polypeptide lacking an apoptotic regulation of targeting (ART) domain. P1 has cytostatic activity and can be used in the modulation of apoptosis. The polypeptides and methods from the present invention are useful for identifying compounds that modulate apoptosis which can then be used for treating cancer. The present sequence represents a mouse BAX peptide sequence of amino acids 1 to 20, which is used in an example from the present invention.

SQ Sequence 20 AA;

Query Match 47.4%; Score 9; DB 21; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 0.027;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPPSSSEQI 19
 Db 11 GGPPSSSEQI 19

RESULT 4
 AAY90738 ID AAY90738 standard; peptide; 20 AA.

AC AAY90738; FT
 XX DE Rat BAX amino acid sequence 1 to 20 SEQ ID NO:4.
 XX DT Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
 KW cell death; cancer; cytostatic.
 XX OS Rattus norvegicus.
 XX PN WO200020446-A2.
 XX PD 13-APR-2000.
 XX PF 05-OCT-1999; 99WO-1B01680.
 XX PR 05-OCT-1998; 98US-0166028.
 PA (UVMC-) UNIV MCGILL.
 XX PT Shore GC, Goping S;
 XX DR WPI; 2000-303740/26.
 PT BX polypeptide lacking an ART domain, useful for identifying agents
 that modulate apoptosis which can then be used for treating cancer -
 PS Example 2; Page 53; 53pp; English.
 CC The present invention describes a pure protein (P1) comprising a BAX
 polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 apoptosis. The polypeptides and methods from the present invention are
 useful for identifying compounds that modulate apoptosis which can then
 be used for treating cancer. The present sequence represents a rat
 BAX peptide sequence of amino acids 1 to 20, which is used in an
 example from the present invention.
 CC Sequence 20 AA:
 XX SQ Query Match Best Local Similarity 100.0%; Score 9; DB 21; Length 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPTSSSEQI 19
 |||||||
 DB 11 GGPRISSSEQI 19
 RESULT 5
 AAY70816
 ID AAY70816 standard; Protein; 70 AA.
 AC AAY70816;
 XX DT 31-JUL-2000 (first entry)
 DE Human neuroprotective truncated BAX protein, tBAX70.
 XX KW human; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 Region 1..58
 /note= "N-terminal region of BAX alpha"
 FT 59..70
 /label= Partial_BH3_domain
 /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"
 FT XX
 FN PN WO200023083-A1.
 XX PR 22-OCT-1999; 99WO-0524747.
 XX PD 27-APR-2000.
 XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -
 PS XX
 XW Claim 4; Page 32; 43pp; English.
 CC The present sequence is a specifically claimed truncated BAX protein
 tBAX70 which inhibits neuronal apoptosis induced by trophic factor
 deprivation. The protein consists of first 70 amino acids of human
 BAX alpha that includes the N-terminal region and a portion of the BH3
 domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 the full-length BAX alpha. The tBAX protein lacking only the
 transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX SQ Query Match Best Local Similarity 100.0%; Score 9; DB 21; Length 70;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPTSSSEQI 19
 |||||||
 Db 11 GGPTSSSEQI 19
 RESULT 6
 AAY70817
 ID AAY70817 standard; Protein; 70 AA.
 AC AAY70817;
 XX DT 31-JUL-2000 (first entry)
 DE Mouse neuroprotective truncated BAX protein, tBAX70.
 XX KW Mouse; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 OS Mus musculus.
 XX PH Key Location/Qualifiers
 Region 1..58
 /note= "N-terminal region of BAX alpha"
 FT Domain 59..70
 /label= Partial_BH3_domain
 /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"
 FT XX
 FN PN WO200023083-A1.
 XX PR 27-APR-2000.
 XX PD

PF 22-OCT-1999; 99WO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Johnson EM, Easton R;
 XX
 DR WPI; 2000-339513/29.
 XX
 PT Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 32; 43pp; English.
 CC The present sequence is a specifically claimed truncated BAX protein tBAX70 which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of first 70 amino acids of mouse BAX alpha, that includes the N-terminal region and a portion of the BH3 domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g., neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.
 CC
 XX Sequence 70 AA;
 SQ Query Match 47.4%; Score 9; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.081; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPISSEQI 19
 Db 11 GGPISSEQI 19

RESULT 7
 AAY70820
 ID AAY70820 standard; Protein; 70 AA.
 XX
 AC AAY70820;
 XX
 DT 31-JUL-2000 (first entry)
 DE Human neuroprotective truncated BAX protein tBAX70 mutant.
 XX
 KW Human; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.
 KW
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..58
 FT /note= "N-terminal region from BAX alpha"
 FT Domain 59..70
 FT /label= Partial.BH3_domain
 FT /note= "BH3 domain in the full-length BAX alpha consists of amino acids 59-73"
 FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"
 FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
 FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
 XX
 PN WO200023083-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 22-OCT-1999; 99WO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.

PR 22-OCT-1998; 98US-0177315.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Johnson EM, Easton R;
 XX
 DR WPI; 2000-339513/29.
 XX
 PT Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 33-34; 43pp; English.
 CC The present sequence is a specifically claimed truncated BAX protein, tBAX70 mutant (tBAX70M) which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of the N-terminal region and a portion of BH3 domain of human BAX alpha. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g., neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.
 CC
 XX Sequence 70 AA;
 SQ Query Match 47.4%; Score 9; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.081; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPISSEQI 19
 Db 11 GGPISSEQI 19

RESULT 8
 AAY70821
 ID AAY70821 standard; Protein; 70 AA.
 XX
 AC AAY70821;
 XX
 DT 31-JUL-2000 (first entry)
 DE Mouse neuroprotective truncated BAX protein tBAX70 mutant.
 XX
 KW Mouse; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..58
 FT /note= "N-terminal region from BAX alpha"
 FT Domain 59..70
 FT /label= Partial.BH3_domain
 FT /note= "BH3 domain in the full-length BAX alpha consists of amino acids 59-73"
 FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"
 FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
 FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
 XX
 PN WO200023083-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 22-OCT-1999; 99WO-US24747.
 XX
 PR 22-OCT-1998; 98US-0177315.

PA (UNIW) UNIV WASHINGTON.
 XX
 PT Johnson EM, Easton R;
 XX DR WPI; 2000-339513/29.
 XX N-PSDB; AAD00124.
 PT truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 34; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX70 mutant (tBAX70M), which inhibits neuronal apoptosis induced by trophic factor
 region and a portion of BH3 domain from mouse BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 SQ Sequence 70 AA;
 Query Match 47.4%; Score 9; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 0.081; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Oy 11 GGPTSSSEQI 19
 |||||||
 Db 11 GGPTSSSEQI 19
 Sequence 78 AA;
 XX
 RESULT 9
 AAY70818
 ID AAY70818 standard; Protein: 78 AA.
 XX AC AAY70818;
 XX DT 31-JUL-2000 (first entry)
 XX DE Human neuroprotective truncated BAX protein, tBAX78.
 XX KW Human; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;
 XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 XX spinal cord injury; head trauma; stroke.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
 FT Region 1..58
 FT /note= "N-terminal region of BAX alpha"
 FT Domain 59..73
 FT /label= BH3_domain
 PN WO200023083-A1.
 XX PD 27-APR-2000.
 XX PF 22-OCT-1999; 99WO-US24747.
 XX PR 22-OCT-1998; 98US-0177315.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PT Johnson EM, Easton R;
 XX DR WPI; 2000-339513/29.
 XX N-PSDB; AAD00123.
 XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 33; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein
 CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 78 amino acids of mouse
 CC BAX alpha, that includes the N-terminal region and BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 RESULT 10
 AAY70819
 ID AAY70819 standard; Protein: 78 AA.
 XX AC AAY70819;
 XX DT 31-JUL-2000 (first entry)
 XX DE Mouse neuroprotective truncated BAX protein, tBAX78.
 XX KW Mouse; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;
 XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 XX spinal cord injury; head trauma; stroke.
 XX OS Mus musculus.
 XX FH Location/Qualifiers
 FT Region 1..58
 FT /note= "N-terminal region of BAX alpha"
 FT Domain 59..73
 FT /label= BH3_domain
 PN WO200023083-A1.
 XX PD 27-APR-2000.
 XX PF 22-OCT-1999; 99WO-US24747.
 XX PR 22-OCT-1998; 98US-0177315.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PT Johnson EM, Easton R;
 XX DR WPI; 2000-339513/29.
 XX N-PSDB; AAD00123.
 XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 33; 43pp; English.
 XX
 CC The present sequence is a specifically claimed truncated BAX protein
 CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 78 amino acids of mouse
 CC BAX alpha, that includes the N-terminal region and BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of

CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

SQ	Sequence	78 AA;
OY	11 GGPSSSEOI 19	47.4%; Score 9; DB 21; Length 78; Best local Similarity 100.0%; Pred. No. 0.089; Mismatches 0; Indels 0; Gaps 0;
Db	11 GGPPSSEQI 19	47.4%; Score 9; DB 21; Length 78; Best local Similarity 100.0%; Pred. No. 0.089; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

ID	AAV70822 standard; Protein; 78 AA.
XX	AAV70822;
AC	AAV70822;
DT	31-JUL-2000 (first entry)
DE	Human neuroprotective truncated BAX protein tBAX78 mutant.
KW	Human; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.
XX	Homo sapiens.
OS	OS Synthetic.
FH	Key Location/Qualifiers
FT	Misc-difference 55 /note= "Wild type Ser is substituted by Ala"
FT	Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
FT	Region 71..78 /note= "sequence not found in BAX alpha"
FT	Region 71..78 /note= "sequence not found in BAX alpha"
PN	WO200023083-A1.
XX	
PD	27-APR-2000.
XX	
PR	22-OCT-1999; 99WO-US24747.
XX	
PR	22-OCT-1999; 99US-0177315.
XX	
PA	(UNIW) UNIV WASHINGTON.
XX	
PI	Johnson EM, Easton R;
XX	
DR	WPI; 2000-339513/29.
XX	
N-PSDB; AAD00125.	
PT	Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
XX	
PS	Claim 4; Page 34; 43pp; English.
XX	
The present sequence is a specifically claimed truncated BAX protein, tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of the N-terminal region and a portion of BH3 domain of human BAX alpha, and a novel C-terminal sequence of 8 amino acids not present in BAX alpha. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.	
CC	Sequence 78 AA;

CC	spinal cord injury, head trauma and stroke.
XX	Sequence 78 AA;
SQ	Sequence 78 AA;

Query Match 47.4%; Score 9; DB 21; Length 78;
Best local Similarity 100.0%; Pred. No. 0.089; Mismatches 0; Indels 0; Gaps 0;

OY	11 GGPPSSEQI 19	47.4%; Score 9; DB 21; Length 78; Best local Similarity 100.0%; Pred. No. 0.089; Mismatches 0; Indels 0; Gaps 0;
Db	11 GGPPSSEQI 19	47.4%; Score 9; DB 21; Length 78; Best local Similarity 100.0%; Pred. No. 0.089; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

ID	AAV70823 standard; Protein; 78 AA.
XX	AAV70823;
AC	AAV70823;
DT	31-JUL-2000 (first entry)
DE	Mouse neuroprotective truncated BAX protein tBAX78 mutant.
KW	Mouse; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.
XX	Mus musculus.
OS	OS Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 55 /note= "Wild type Ser is substituted by Ala"
FT	Misc-difference 60 /note= "Wild type Ser is substituted by Ala"
FT	Region 71..78 /note= "sequence not found in BAX alpha"
FT	Region 71..78 /note= "sequence not found in BAX alpha"
PN	WO200023083-A1.
XX	
PD	27-APR-2000.
XX	
PR	22-OCT-1999; 99WO-US24747.
XX	
PR	22-OCT-1999; 99US-0177315.
XX	
PA	(UNIW) UNIV WASHINGTON.
XX	
PI	Johnson EM, Easton R;
XX	
DR	WPI; 2000-339513/29.
XX	
N-PSDB; AAD00126.	
XX	
PT	Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
XX	
PS	Claim 4; Page 34-35; 43pp; English.
CC	The present sequence is a specifically claimed truncated BAX protein, tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of the N-terminal region and a portion of BH3 domain of mouse BAX alpha, and a novel C-terminal sequence of 8 amino acids not present in BAX alpha. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.
SQ	Sequence 78 AA;

Query Match		Score	DB	Length
Best Local Similarity		100.0%	Pred. No.	0.089;
Matches		9;	Conservative	0;
Qy	ID	GGPTSSSEQI	19	
Db	ID	GGPTSSSEQI	19	
RESULT 13				
AAY34149	AAY34149	standard:	Protein:	131 AA.
XX	XX			
AC	AAY34149;			
XX	XX			
DT	30-NOV-1999	(first entry)		
XX				
DE	Human truncated Bax protein.			
XX				
KW	Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.			
XX				
OS	Homo sapiens.			
XX				
FH	Key Location/Qualifiers			
Domain	59..101 "Portion of BH3 domain essential for dimerisation"			
FT	/note=			
XX				
PN	W09946371-A2.			
XX				
PD	16-SEP-1999.			
XX				
PF	99WO-US05359.			
XX				
PR	11-MAR-1998; 98US-0077541.			
XX				
PA	(TEXA) UNIV TEXAS SYSTEM.			
XX				
PI	McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;			
PI	Ji L, Roth JA;			
XX				
DR	WPI; 1999-551404/46.			
DR	N-PSDB: AAZ19763.			
XX				
PT	New adenovirus vectors, used for killing or inhibiting the growth of			
PT	cells and for treating cancers			
XX				
PS	Claim 26; page 148-149; 151pp; English.			
CC	This sequence represents a human truncated Bax protein. The cDNA contains a single base deletion relative to the wild-type (AAZ19764), causing a frameshift which leads to translation of a premature stop codon resulting in a truncated protein. However, the domain responsible for its function is still present in the truncated protein. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the expression of Bax is upregulated at the transcriptional level by p53, and Bax mRNA and protein expression have been shown to increase following induction of p53. Bax protein can function as a homodimer, or it can heterodimerise with other Bcl-2 gene family members such as the antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members provides a means of controlling cell death via the "rheostat" model. This model suggests that the relative amounts of Bcl-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing this Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.			
CC				
XX	Sequence	131 AA;		
SQ				
Query Match	Score	DB	Length	
Best Local Similarity	100.0%	Pred. No.	0.14;	
Matches	9;	Conservative	0;	Mismatches
Qy	ID	GGPTSSSEQI	19	
Db	ID	GGPTSSSEQI	19	
RESULT 14				
AAR14006	AAR71405	standard;	Protein:	192 AA.
XX				
AC	AAR71405;			
XX				
DT	15-NOV-1995 (first entry)			
XX				
DE	Human Bax protein.			
XX				
KW	Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line; proliferation; membrane-associated cytoplasmic protein; B cell; T cell; apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.			
XX				
OS	Homo sapiens.			
XX				
PF	W099505750-A.			
XX				
PD	02-MAR-1995.			
XX				
PF	24-AUG-1994; 94WO-US09701.			
XX				
PI	Korsmeyer SU;			
XX				
PR	W099505750-A.			
XX				
PR	26-AUG-1993; 93US-0112208.			
XX				
PR	25-MAY-1994; 94US-0248819.			
XX				
PA	(UNIV) UNIV WASHINGTON.			
XX				
PT	Methods for producing and identifying mutant bcl-2 proteins -			
PT	that lack death repressor activity and/or lacks binding to Bax.			
XX				
PS	Disclosure; Fig 3; 133pp; English.			
XX				
CC	This sequence represents human Bax protein. Bax is a protein which is associated with the human bcl-2 alpha and beta proteins, the sequences of which are given in AAR71404-05 respectively. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T origins rather than directly promoting proliferation of these cell types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose response to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death following an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion in the BH1 or BH2 domains. This makes the mutant protein substantially incapable of binding Bax and/or incapable of death repressor activity. Down regulation of bcl-2 is useful in cancer therapy, controlling hyperplasias and eliminating self-reactive clones in autoimmunity by favouring death effector molecules. Up			

CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.
 XX
 SQ Sequence 192 AA;
 Query Match 47.4%; Score 9; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0;
 QY 11 GGPPSSEQI 19
 |||||||||
 Db 11 GGPPSSEQI 19

RESULT 15
 AAR1407
 ID AAR1407 standard; Protein; 192 AA.
 XX
 AC AAR1407;
 XX
 DT 15-NOV-1995 (first entry)
 XX
 DE Murine Bax protein.
 XX
 KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
 KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KW ischaemic cell death.
 XX
 OS Mus musculus.
 XX
 PN W09505750-A.
 XX
 PD 02-MAR-1995.
 XX
 PF 24-AUG-1994; 94WO-US09701.
 XX
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1995-106605/14.
 XX
 PT Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 XX
 PS Disclosure; Fig 3; 133pp; English.
 XX

This sequence represents murine Bax protein. Bax is a protein which is associated with the bcl-2 alpha and beta proteins. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated cytosolic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T origins rather than directly promoting proliferation of these cell types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose response to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death following an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion in the BH1 or BH2 domains. This makes the mutant protein substantially incapable of binding Bax and/or incapable of death repressor activity. Down regulation of bcl-2 is useful in cancer therapy, controlling hyperplasias and eliminating self-reactive

CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.
 XX
 SQ Sequence 192 AA;
 Query Match 47.4%; Score 9; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0;
 QY 11 GGPPSSEQI 19
 |||||||||
 Db 11 GGPPSSEQI 19

Search completed: January 7, 2003, 12:38:30
 Job time : 31.2051 secs

CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.
 XX
 SQ Sequence 192 AA;
 Query Match 47.4%; Score 9; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0;
 QY 11 GGPPSSEQI 19
 |||||||||
 Db 11 GGPPSSEQI 19

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:36:33 ; Search time 25.641 Seconds

{without alignments} 160.717 Million cell updates/sec

Title:

0S-09-876-204-3

Perfect score:

20 1 MDGSEQPRGGPPTSEQIM 20

Sequence:

09tktv0 nephrosetlin

09yf73 drosophila

012583 candida mal

01tsv9 hom sapien

0910x8 human astro

09ye12 aeropyrum p

09fpb4 oryza sativ

081993 kalanchoe f

09hbro hom sapien

08wrt5 hom sapien

09rc72 bacillus ha

094i13 oryza sativ

043770 homo sapien

08wuzo hom sapien

088664 mus musculu

08vx68 solenangis

08vxn2 cupressus s

08vya3 taxus sp. h

08wp2 annas comb

08vxg5 leptotes bi

09fiq4 thermus the

09je41 herpesvirus

09v3w7 drosophila

09m476 dendrobium

09bvvs5 homo sapien

088107 xenopus lae

09034 trichodermia

086566 hydrella ve

09nx73 homo sapien

Searched:

671580 seqs, 206047115 residues

Word size :

0

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

- 1: SPTRMBL_21:*
- 2: SP_archea:*
- 3: SP_bacteria:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rabbit:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_rvirus:*
- 16: SP_bacteriaph:*
- 17: SP_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	20	100.0	24	4 Q8WXL1	Q8WXL1 hom sapien
2	20	100.0	164	6 Q9UQD6	Q9UQD6 homo sapien
3	20	100.0	179	4 Q9NRG7	Q9NRG7 homo sapien
4	60.0	192	6 Q8SO43	Q8SO43 felis silve	
5	10	50.0	24	11 Q8HYH7	Q8HYH7 mus musculu
6	45.0	743	10 Q9M221	Q9M221 arabidopsis	
7	8	40.0	531	4 Q9Y3X0	Q9Y3X0 homo sapien
8	7	35.0	11 Q9R0K9	Q9R0K9 mus musculu	
9	7	35.0	5 Q9N357	Q9N357 caenorhabdi	
10	7	35.0	541	10 Q9S7V5	Q9S7V5 arabi dopsis
11	7	35.0	589	5 Q9B658	Q9B658 trypanosoma
12	7	35.0	748	0 Q9W2R7	Q9W2R7 oriza sativ
13	7	35.0	968	3 P87199	P87199 ustilago ma
14	7	35.0	1217	4 Q60336	Q60336 homo sapien
15	6	30.0	4 Q9H039	Q9H039 homo sapien	
16	6	30.0	60	16 Q93JL2	Q93JL2 streptomyce

RESULT 1

Q8WXL1

PRELIMINARY;

PRT;

24 AA.

ID

Q8WXL1;

DT

01-MAR-2002

(TREMBREL_20, Last sequence update)

DT

01-MAR-2002

(TREMBREL_20, Last annotation update)

DE

BC12-associated X protein (Fragment).

GN

BAX.

OS

Homo sapiens (Human).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;

OX

NCBI_TaxID=9606;

RN

[1]

SEQUENCE FROM N.A.

RA

Thornborrow E.C., Schwartzfarb E.M., Manfredi J.J.:

"A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";

RT

Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AR339054; AAL7333.1; -

FT

NOLTER

24 AA;

2379 MW;

8C3D3EB8B7479B798 CRC64;

ALIGNMENTS

Q8WXL1

PRELIMINARY;

PRT;

164 AA.

ID

Q8WXL1;

AC

Q9N357

PPRELIMINARY;

PRT;

164 AA.

ID

Q8WXL1;

AC

Q9N357

PPRELIMINARY;

PRT;

164 AA.

ID

Q8WXL1;

AC

Q9N357

PPRELIMINARY;

PRT;

164 AA.

ID

Q8WXL1;

PPRELIMINARY;

PRT;

164 AA.

ID

Q8WXL1;

RESULT 2

Q9QD6

PPRELIMINARY;

PRT;

164 AA.

ID

Q9QD6

PPRELIMINARY;

DT

01-MAY-2000

((TREMBREL_13, Last sequence update))

DT

01-MAY-2000

((TREMBREL_13, Last annotation update))

DT

01-JUN-2002

DT

01-JUN-2002

((TREMBREL_21, Last annotation update))

DE	Bax epsilon;	ID	Q85043	PRELIMINARY;	PRT;	192 AA.	
OS	Homo sapiens (Human);	AC	Q85043;				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	ID	Q85043;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DT	01-JUN-2002 (TREMBrel. 21, Last sequence update)				
NCBI_TaxID=9606;	[1]	DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)				
RN	SEQUENCE FROM N.A.	DE	Bax protein.				
RP	TISSUE=BRAIN;	GN	BAX				
RX	Medline=99120940; PubMed=9920818;	OS	Felis silvestris catus (Cat).				
RA	Shi, B.; Tribe D.; Kajiji S.; Iwata K.K.; Bruskin A.; Mahajna J.;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
RT	"Identification and characterization of baxepsilon, a novel bax variant missing the BH2 and the transmembrane domains.";	OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
RT	Biophys. Res. Commun. 254:779-785(1999).	OX	Yamazaki J., Oguma K., Kano R., Hasegawa A.;				
RL	EMBL; AB07826; ADD2706.1.;	RA	"molecular cloning of the feline bcl-2 family.";				
DR	InterPro; IPR000712; BCL2_BH.	RT	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.				
DR	InterPro; IPR002475; BCL2_family.	DR	EMBL; AB080724; BAB85810.1.;				
PFAM	PF00452; BCL-2; 1.	DR	EMBL; AB080724; BAB85810.1.;				
SMART	SM00337; BCL; 1.	SEQUENCE	192 AA; 2132 MW; 852D271AE8923FB CRC64;				
DR	PROSITE; PS50062; BCL2_FAMILY; 1.	Db	1 MDGSGEQPREGG 12				
DR	PROSITE; PS01080; BH1; 1.	Query Match	60.0%; Score 12; DB 6; Length 192;				
DR	PROSITE; PS01259; BH3; 1.	Best Local Similarity	100.0%; Pred. No. 2.3e-05;				
SEQUENCE	164 AA; 18129 MW;	Matches	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 MDGSGEQPREGG 12	Db	1 MDGSGEQPREGG 12				
QY	1 MDGSGEQPREGG 12	Query Match	60.0%; Score 12; DB 6; Length 192;				
QY	1 MDGSGEQPREGG 12	Best Local Similarity	100.0%; Pred. No. 2.3e-05;				
Db	1 MDGSGEQPREGG 12	Matches	0; Mismatches 0; Indels 0; Gaps 0;				
RESULT	3	RESULT	5	RESULT	5	RESULT	6
Q9NYG7	PRELIMINARY;	Q9NYG7	PRELIMINARY;	Q8VWY7	PRELIMINARY;	Q8VWY7	PRELIMINARY;
ID	PRT; 179 AA.	ID	PRT; 24 AA.	ID	PRT; 24 AA.	ID	PRT; 743 AA.
AC		AC		AC		AC	
AC		DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)	DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)	DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)	DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)	DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)	DE	Bcl-2-associated X protein (Fragment).	DE	Bcl-2-associated X protein (Fragment).	DE	Bcl-2-associated X protein (Fragment).
DE	Bax-sigma.	GN	BAX	GN	BAX	GN	BAX
OS	Homo sapiens (Human).	OS	Mus musculus (Mouse).	OS	Mus musculus (Mouse).	OS	Mus musculus (Mouse).
OC	Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	NCBI_TaxID=9606;	RN	[1]	NCBI_TaxID=10090;	RN	NCBI_TaxID=10090;	RN
RC	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RA	STRAIN=BALB/C;	RA	Thornborow E.C., Schwartzfarb E.M., Manfredi J.J.;	RA	Thornborow E.C., Schwartzfarb E.M., Manfredi J.J.;
RX	Medline=20237095; PubMed=1072918;	RT	"A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";	RT	"A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";	RT	"A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
RA	Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RA	"Characterization of bax-sigma, a cell death-inducing isoform of Bax.";	RT	EMBL; AF339055; AAL7334.1.;	RT	EMBL; AF339055; AAL7334.1.;	RT	EMBL; AF339055; AAL7334.1.;
RT	Biochem. Biophys. Res. Commun. 270:868-879(2000).	RL	NON_TER 24 24	RL	NON_TER 24 24	RL	NON_TER 24 24
DR	EMBL; AF247393; AF71267.1.;	DR	SEQUENCE 24 AA; 2326 MW;	DR	SEQUENCE 24 AA; 2326 MW;	DR	SEQUENCE 24 AA; 2326 MW;
DR	InterPro; IPR00712; Bcl2_BH.	DR	998C7E8B7479A6CC CRC64;	DR	998C7E8B7479A6CC CRC64;	DR	998C7E8B7479A6CC CRC64;
DR	InterPro; IPR002475; BCL2_FAMILY.	DR	Query Match	Query Match	Query Match	Query Match	Query Match
DR	Biochem. Biophys. Res. Commun. 270:868-879(2000).	DR	Best Local Similarity 100.0%; Pred. No. 0.005;	DR	Best Local Similarity 100.0%; Pred. No. 0.005;	DR	Best Local Similarity 100.0%; Pred. No. 0.005;
DR	SMART; SM00337; BCL; 1.	DR	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	PROSITE; PS50062; BCL2_FAMILY; 1.	DR	Db	Db	Db	Db	Db
DR	PROSITE; PS01080; BH1; 1.	DR	11 GGPPSSEQM 20	DR	11 GGPPSSEQM 20	DR	11 GGPPSSEQM 20
DR	PROSITE; PS01259; BH3; 1.	DR	11 GGPPSSEQM 20	DR	11 GGPPSSEQM 20	DR	11 GGPPSSEQM 20
SEQUENCE	179 AA; 19718 MW;	SQ	5802B0ACT3B2E4CE CRC64;	SQ	5802B0ACT3B2E4CE CRC64;	SQ	5802B0ACT3B2E4CE CRC64;
QY	100.0%; Score 20; DB 4; Length 179;	QY	100.0%; Score 10; DB 11; Length 24;	QY	50.0%; Score 10; DB 11; Length 24;	QY	50.0%; Score 10; DB 11; Length 24;
Best Local Similarity	100.0%; Pred. No. 5.2e-14;	Best Local Similarity	100.0%; Pred. No. 0.005;	Best Local Similarity	100.0%; Pred. No. 0.005;	Best Local Similarity	100.0%; Pred. No. 0.005;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MDGSGEQPREGGGPSSSEQM 20	OY	1 MDGSGEQPREGGGPSSSEQM 20	OY	1 MDGSGEQPREGGGPSSSEQM 20	OY	1 MDGSGEQPREGGGPSSSEQM 20
Db	1 MDGSGEQPREGGGPSSSEQM 20	Db	1 MDGSGEQPREGGGPSSSEQM 20	Db	1 MDGSGEQPREGGGPSSSEQM 20	Db	1 MDGSGEQPREGGGPSSSEQM 20
RESULT	4	Q85043		Q85043		Q85043	
Q85043							

RESULT 10
 09SV5 PRELIMINARY; PRT; 541 AA.
 ID 09SV5
 AC 09SV5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE T16011.4 protein (NP3G09000/R16011.4).
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.,
 RT "Arabidopsis thaliana chromosome III BAC T16011 genomic sequence.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.,
 RT "Arabidopsis thaliana chromosome III BAC T16011 genomic sequence.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam J.M., Lin J., Liu S.K., Miranda M., Narukawa M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC010871; AF078271; -;
 DR EMBL; AC009326; AD563161; -;
 DR EMBL; AF428216; AA1161081; -;
 SQ SEQUENCE 541 AA; 3AREEL5AD4EADAE CRC64;

Query Match 35.0%; Score 7; DB 10; Length 541;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RGSGPTA 15
 I|||||
 Db 342 RGSGPTA 348

RESULT 11
 0.8658 PRELIMINARY; PRT; 589 AA.
 ID 018658
 AC 018658;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
 DE PAR3.
 GN PAR3B OR PAR3C OR PAR3A.
 OC Trypanosoma cruzi
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ESMERALDO;
 RA =Fouts D.L., Miller M.J., Manning J.E.;

RESULT 12
 Q8W2R7 PRELIMINARY; PRT; 748 AA.
 ID Q8W2R7
 AC Q8W2R7;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 RL Putative wall associated protein kinase.
 RN OS OSNBA0028C16.5.
 RP SEQUENCE FROM N.A.
 RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
 RA Sasaki C., Henry D., Oates R., Simmons J.;
 RT "Rice Genomic Sequence.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC098565; AA169424.1; -;
 DR InterPro; IPRO00152; Ask_hydroxyl.
 DR InterPro; IPRO00561; EGF_like.
 DR InterPro; IPRO01881; EGF_Ca.
 DR InterPro; IPRO00719; Euk_pk kinase.
 DR InterPro; IPRO02290; Ser-thr_pk kinase.
 DR InterPro; IPRO01245; Tyr_pk kinase.
 DR InterPro; IPRO01245; Tyr_pk kinase.
 DR ProDom; PD000001; Euk_pk kinase; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00001; EGF_like; 2.
 DR SMART; SM00220; S_TK_C; 1.
 DR SMART; SM00219; Tyr_C; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00187; EGF_CA; UNKNOWN_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50018; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW Kinase.
 SQ SEQUENCE 748 AA; 82540 MW; 50BF15F0791AA12E CRC64;

Query Match 35.0%; Score 7; DB 10; Length 748;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QPRGGP 13
 I|||||
 Db 343 QPRGGP 349

RESULT 13
 P87199 PRELIMINARY; PRT; 968 AA.
 ID P87199
 AC P87199;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DR Kinesin motor protein.

QY 4 SGEPORG 10
 QY 4 SGEPORG 10
 Db 838 SGEPORG 844

GN KIN2.
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 NCBI_TaxID=5270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97361828; PubMed=9218789;
 RA Lehmler C., Steinberg G., Snetselaar K.M., Schliwa M., Kahmann R.,
 Bolker M.,
 RT "Identification of a motor protein required for filamentous growth in
 Ustilago maydis.";
 RL EMBO J. 16:3464-3473(1997).
 DR EMBL: 092845; AAC63337.1; -.
 HSSP: P33176; 1B62.
 DR InterPro; IPR001752; kinesin_motor.
 PRIM; PF00225; kinesin; 1.
 DR SMART; SM0129; KISC; 1.
 DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.
 SQ SEQUENCE 968 AA; 107472 MW; 3A3B282020D298ED CRC64;

Query Match 35.0%; Score 7; DB 3; Length 968;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 RGGPTS 15
 Db 921 RGGPTS 927

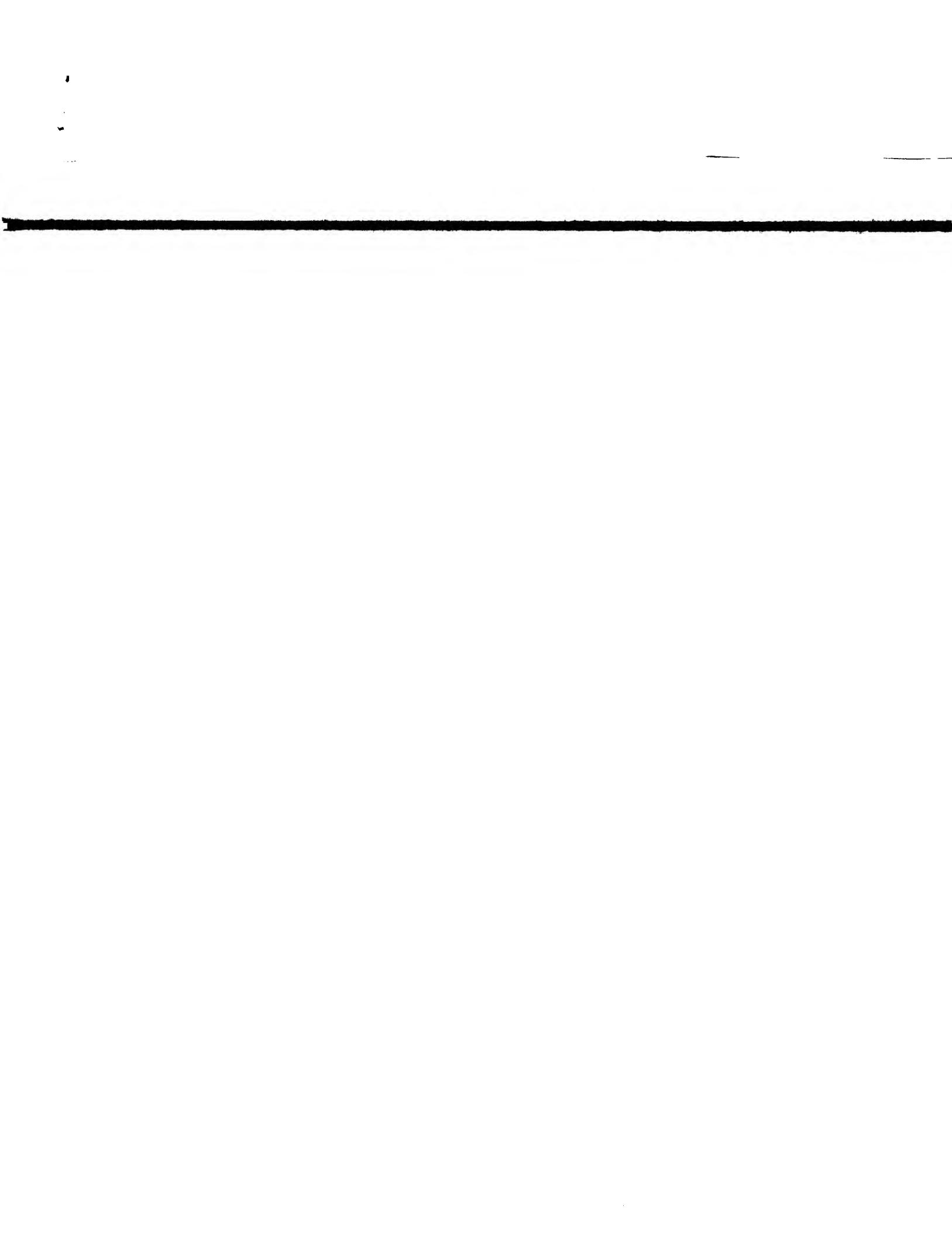
RESULT 14
 OR0336 PRELIMINARY; PRT; 1217 AA.
 ID 060336; AC 060336;
 DT 01-AUG-1998 (TREMBrel. 07, Created)
 DT 01-AUG-1998 (TREMBrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE KIAA0596 protein (Fragment).
 GN KIAA0596.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Boecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
 DR Submitted (DDC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL51276; CRC21671.1; -.
 DR KIAA0596 protein (Fragment).
 FT NON_TER 1
 SQ SEQUENCE 45 AA; 5069 MW; 64557BA7DB929BB7 CRC64;

Query Match 30.0%; Score 6; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 TSSEBQI 19
 Db 1 TSSEBQI 6

Search completed: January 7, 2003, 12:39:50
 Job time : 26.641 secs

RC TISSUE=BRAIN;
 RX MEDLINE=98390545; PubMed=9528581;
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 RA Chara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 The complete sequences of 100 new cDNA clones from brain which can
 code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC "SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR AB011168; BA22522.1; -.
 DR InterPro; IPR002114; HPR_Serp_site.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF0040; WD40; 8.
 DR PRINTS; PRO0320; GPROMEINBPRP.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR InterPro; IPR002114; HPR_Serp_site.
 DR PROSITE; PS50291; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER 1
 SQ SEQUENCE 1217 AA; 131098 MW; 0BC4E4C66722BFF5 CRC64;

Query Match 35.0%; Score 7; DB 4; Length 1217;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



				GenCore version 5.1.3
Copyright (c) 1993 - 2003				Compugen Ltd.
On protein - protein search, using sw model				
Run on:	January 7, 2003, 12:31:53 ; Search time 7.17949 Seconds			
	(without alignments)			
	115.541 Million cell updates/sec			
Title:	US-09-876-204-3			
Perfect score:	20			
Sequence:	1 MDGSGEQPRGGGPTTSEQIM 20			
Scoring table:	OLIGO			
	Gapop 60.0 , Gapext 60.0			
Searched:	112892 seqs, 41476328 residues			
Word size :	0			
Total number of hits satisfying chosen parameters:	112892			
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Post-processing: Listing first 45 summaries				
Database :	SwissProt_40; *			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
	SUMMARIES			
Result No.	Score	Query Length	DB ID	Description
1	20	100.0	143 1	BAXD_HUMAN
2	20	100.0	192 1	BAXA_BOVIN
3	20	100.0	192 1	BAXA_HUMAN
4	20	100.0	218 1	BAXC_HUMAN
5	11	55.0	41 1	BAXA_RAT
6	7	10	192 1	BAXA_MOUSE
8	8	6	105 1	YGRM_MICRO
9	9	6	120 1	NJ3C_NEFL
10	10	6	126 1	SM01_CABEL
11	11	6	218 1	RRA5_MOUSE
12	12	6	30.0 1	ASPX_HUMAN
13	6	30.0	265 1	Y3K_HUMAN
14	6	30.0	298 1	FSA_SHEEP
15	15	6	337 1	FSA_BOVIN
16	16	6	344 1	FSA_HORSE
17	17	30.0	344 1	FSA_PIG
18	18	6	344 1	PCK_MCYCLE
19	19	6	416 1	CP5G_CANTR
20	20	6	30.0 1	HS74_PARLI
21	21	6	30.0 1	CP5L_DEBHA
22	22	6	519 1	CAP1_SORBI
23	23	6	519 1	CP5M_DEBHA
24	24	6	30.0 1	CP5I_CANNMA
25	25	6	639 1	CP5F_CANTR
26	26	6	30.0 1	SYM_PODAN
27	27	6	680 1	YKL1_YEAST
28	28	6	30.0 1	DML1_ARATH
29	29	6	970 1	PROST1_ARATH
30	30	6	960 1	CAP2_MESSR
31	31	6	30.0 1	CAP2_SORBI
32	32	6	960 1	CP5804_sorghum_bic
33	33	6	30.0 1	CAPP_PICAB
			963	P51063_picea_abies
				ALIGNMENTS
				RESULT 1
			BAXD_HUMAN	STANDARD; PRT: 143 AA.
			ID: BAXD_HUMAN	
			AC: P5259;	
			DT: 01-OCT-1996 (Rel. 34, Created)	
			DT: 01-OCT-1996 (Rel. 34, Last sequence update)	
			DT: 15-JUN-2002 (Rel. 41, Last annotation update)	
			DE: BAX protein, cytoplasmic isoform delta.	
			GN: BAX.	
			OS: Homo sapiens (Human).	
			OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo.	
			RN: NCBI_TaxID:9606;	
			RP: [1]	
			SEQUENCE FROM N.A.	
			RX: MEDLINE=95331797; PubMed=7607695;	
			RA: Apté S. S.; Mattiel M.-G.; Olsen B. R.	
			"Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a novel alternatively spliced transcript, BAX delta."	
			RL: Genomics 26: 93-94 (1995).	
			CC: -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).	
			CC: -!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPlicing.	
			CC: -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.	
			CC: -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.	
			CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
			CC: EMBL: U19599; AAC50142.1; -	
			DR: Genew; HGNC: 959; BAX.	
			MM: 600040; -	
			DR: InterPro; IPR002475; BCL2_family.	
			DR: InterPro; IPR000712; Bcl12_BH.	
			DR: Pfam; PF00452; Bcl1-2; 1.	
			DR: SMART; SM00337; BCL1.	
			DR: PROSITE; PS01080; BH1; 1.	
			DR: PROSITE; PS01258; BH2; 1.	
			DR: PROSITE; PS50062; BCL2_FAMILY; 1.	
			KW: Apoptosis; Alternative splicing	
			FT: DOMAIN 69	
			FT: DOMAIN 101	
			FT: DOMAIN 116	
			FT: DOMAIN BH2.	
		SEQUENCE	143 AA: 15772 MW; BADF4D71D06A75AB CRC64;	
		Query Match	100.0%; Score 20; DB 1; Length 143;	
		Best Local Similarity	100.0%; Pred. No. 9.1e-14;	
		Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		OY	1 MDGSGEQPRGGGPTTSEQIM 20	

Db	Qy	Best Local Similarity	Pred. No.	Indels	Gaps		
		Matches	20;	Conservative	0;	Mismatches	0;
RESULT 2	1 MDGSQEPRGGGTSSEQIM 20		100.0%	0	0	0	0
BAXA_BOVIN	STANDARD;	PRT;	192 AA.				
ID 002703;	15-JUL-1999 (Rel. 38, Created)						
DT 15-JUN-2002 (Rel. 41, Last annotation update)							
DE Apoptosis regulator BAX, membrane isoform alpha.							
GN BAX.							
OS Bos taurus (Bovine).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.							
OC NCBI_TaxID=9913;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=Holstein; TISSUE=Thymus;							
RX MEDLINE=98162580; PubMed=9501056;							
RA Reyes R.A.; Cockrell G.L.;							
RT "Increased ratio of bcl-2/bax expression is associated with bovine leukemia virus-induced leukemogenesis in cattle.";							
RL Virology 242:184-192 (1998).							
CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE CESSION OF SPERM PRODUCTION (BY SIMILARITY).							
CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERO DIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).							
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).							
CC -!- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE SPLICING.							
CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.							
CC APOTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).							
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY (BH1) DOMAIN.							
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.							
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.							
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.							
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CC -----							
DR EMLU: U92569; AAC88806 1; -.							
DR HSSP; Q07817; IMA2.							
DR InterPro; IPR002415; BCL2_familly.							
DR InterPro; IPR000712; BCL2_BH.							
DR Pfam; PF00452; Bcl-2_1.							
DR SMART; SM00337; BCL_1.							
DR PROSITE; PS01080; BH1; 1.							
DR PROSITE; PS0125; BH2; 1.							
DR PROSITE; PS01259; BH3; 1.							
DR PROSITE; PS0062; BCL2_FAMILY; 1.							
DR Apoptosis; Transmembrane; Alternative splicing.							
FT DOMAIN 59 73 BH3.							
FT DOMAIN 98 118 BH1.							
FT DOMAIN 150 165 BH2.							
FT TRANSMEM 172 192 POTENTIAL.							
SQ SEQUENCE 192 AA; 21259 MW; 6B4D5BABF1D5F87E CRC64;							
Query Match 100.0% Score 20; DB 1; Length 192;							

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DR EMBL; L2475; AAA03621.1; -
DR Genew; HGNC; 959; BAX.
DR MIM; 600040; -;
DR KW Apoptosis; Alternative splicing
DR SEQUENCE; 41 AA; 4678 MW; D94639AABB927859 CRC64;
DR SQ 1 MDGSQEOPRG 11
DR 1 MDGSQEOPRG 11

RESULT 6

BAXA_RAT

ID BAXA_RAT STANDARD PRT: 192 AA.

AC 062995; 063838;

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator BAX, membrane isoform alpha.

GN BAX.

OS Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OOC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TAXID=10116;

[1]

RP MEDLINE:9617871; PubMed=8600029;
RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
RT "The E1B 19K protein blocks apoptosis by interacting with and inhibiting the p53-inducible and death-promoting Bax protein.";
RL Genes Dev. 10:461-477(1996).
[2]
SEQUENCE FROM N.A.

RP TISSUE=Brain; RX MEDLINE:97141318; PubMed=8994223;

RA Madison D.L., Pfeiffer S.E.;
RT "Cloning of the 3'-end of rat bax-alpha and corresponding developmental down-regulation in differentiating primary, cultured oligodendrocytes.";
RT Neurosci. Lett. 220:183-186(1996).
RN [3]
SEQUENCE OF 37-169 FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Ovary;
MEDLINE:95120487; PubMed=7828536;

RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.";
RT Endocrinology 136:232-241 (1995).

-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

-!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.

-!- SUBCELLULAR LOCATION: Membrane-bound.

-!- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE SPlicing.

-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH

RESULT 7

BAXA_MOUSE

ID BAXA_MOUSE STANDARD PRT: 192 AA.

AC 007813;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator BAX, membrane isoform alpha.

GN BAX.

OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OOC Mammalia; Buterilia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TAXID=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6 X DBA/2;

RX MEDLINE:93364978; PubMed=8358790;

RA Oltvai Z.N., Millman C.L., Korsmeyer S.J.;

RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death.";
RL Cell 74:609-619(1993).

HIGHEST LEVELS IN THE TESTIS AND OVARY.

CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.

CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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DR EMBL; U49729; AAC26327.1; -
DR SMART; SMD0337; BCL_1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR InterPro; IPR003475; BCL2_family.Y.
DR InterPro; IPR000712; Bcl12_BH.
DR Pfam; PF0052; Bcl1-2; 1.
DR SMART; SMD0337; BCL_1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT CONFLICT 72 72 S -> N (IN REF. 3).
FT CONFLICT 76 76 L -> M (IN REF. 2).
FT CONFLICT 126 126 C -> Y (IN REF. 2).
FT CONFLICT 149 149 L -> F (IN REF. 3).
FT CONFLICT 159 159 D -> E (IN REF. 1).
SQ SEQUENCE 192 AA; 21350 MW; 7B3CD198D56DF599 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GGGPISSEQIM 20
Db 10 GGGPISSEQIM 20

Db 33 PRGGP 38

RN [1] ||||| Cell 48:137-146(1987).

RN [2] Sequence FROM N.A.

RP TISSUE=Brain, and Uterus;

RC Strausberg R.;

RA Submitted (Oct-2001) to the EMBL/GenBank/DDJB databases.

RL -!- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY WITH ATTACHMENT REQUIRING ACTIVATION OF THE C-TERMINAL CYSTEINE (BY SIMILARITY WITH RAS).

DT -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.

ID SMDLCAEEL STANDARD; PRT; 126 AA.

AC 01/0013; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Probable small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1) (Sm-D1).

DE T2B9_10.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Plectoderrinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1] Sequence FROM N.A.

RP STRAIN=Bristol N2;

RA Fulton L.;

CC Submitted (JUN-1995) to the EMBL/GenBank/DDJB databases.

CC -!- FUNCTION: ESSENTIAL FOR PRE-mRNA SPlicing. IMPLICATED IN THE FORMATION OF STABLE, BIOLOGICALLY ACTIVE SNRNP STRUCTURES (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Nuclear. (By similarity).

CC -!- SIMILARITY: BELONGS TO THE SNRNP CORE PROTEIN FAMILY.

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CC EMBL; M14949; AAA0256_1; -.

CC DR EMBL; M14949; AAA0256_1; JOINED.

CC DR BC016246; AAH16386_1; -.

CC DR BC016318; AAH16318_1; -.

CC DR PIR; A26159; TVHURR.

CC DR HSSP; P01112; IPLL.

CC DR SWISS-2DPAGE; P10301; HUMAN.

CC DR Genew; HGNC:1047; RRAS.

CC DR MIM:165090; -.

CC DR InterPro; IPR001230; Prenyl_Ras.

CC DR InterPro; IPR001806; Ras_transfrring.

CC DR InterPro; IPR005225; Small_GTP.

CC DR Pfam; PF00071; Ras_1.

CC DR PRINTS; PRO0449; RASTRNSFRMNG.

CC DR SMART; SM00173; RAS_1.

CC DR TIGRFAM5; TIGR00231; small_GTP; 1.

CC KW GTP-binding; Prenylation; Lipoprotein.

FT NP_BIND 36 43 GTP (BY SIMILARITY).

FT NP_BIND 83 87 GTP (BY SIMILARITY).

FT NP_BIND 142 145 GTP (BY SIMILARITY).

FT DOMAIN 58 66 EFFECTOR_REGION (BY SIMILARITY).

FT LIPID 215 215 GERANYL-GERANYL (BY SIMILARITY).

SQ SEQUENCE 218 AA; 23480 MW; 437F73I706/0EB28 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 126;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRGGP 13

Db 119 PRGGP 124

RESULT 11

RN RRS_HUMAN STANDARD; PRT; 218 AA.

ID RRS_HUMAN STANDARD; PRT; 218 AA.

AC P10301; 01-MAR-1980 (Rel. 10, Created)

DT 01-MAR-1980 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ras-related protein R-Ras (p23).

GN RROS.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

[1] Sequence FROM N.A.

RX MEDLINE:87078390; PubMed=3098437;

RA Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L., Goeddel D.V.;

RT "Structure of the human and murine R-ras genes, novel genes closely related to ras proto-oncogenes.",

Db 33 PRGGP 38

RN [1] ||||| Cell 48:137-146(1987).

RN [2] Sequence FROM N.A.

RP TISSUE=Brain, and Uterus;

RC Strausberg R.;

RA Submitted (Oct-2001) to the EMBL/GenBank/DDJB databases.

RL -!- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY WITH ATTACHMENT REQUIRING ACTIVATION OF THE C-TERMINAL CYSTEINE (BY SIMILARITY WITH RAS).

DT -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.

ID SMDLCAEEL STANDARD; PRT; 218 AA.

AC P10833; 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Ras-related protein R-Ras (p23).

GN RROS.

OS Mus musculus (Mouse).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP Sequence FROM N.A.

RX MEDLINE:87078390; PubMed=3098437;

RA Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L., Goeddel D.V.;

RT "Structure of the human and murine R-ras genes, novel genes closely related to ras proto-oncogenes.",

RL	Biol. Reprod.	49:316-325(1993).
CC	[4]	-!- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY WITH ATTACHMENT REQUIRING ACYLATION OF THE C-TERMINAL CYSTEINE
CC	CC	(BY SIMILARITY WITH RAS).
CC	CC	-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	CC	-----
DR	EMBL; M21019; AAA40038; 1; -.	
DR	HSSP; P0112; IPI1L.	
DR	MGD; M3J; 98179; Rras.	
DR	InterPro; IPR003577; Gtpase_Ras.	
DR	InterPro; IPR001230; prenyl_site.	
DR	InterPro; IPR001806; Ras_transfmrng.	
DR	InterPro; IPR005225; Small_GTP.	
PRINTS	Pf00071; ras; 1.	
DR	PRINTS; PRO00449; RASTRNSFRNG.	
DR	SMART; SM00173; RAS; 1.	
KW	TIGRFAMS; TIGR00331; small_GTP; 1.	
FT	GTP-binding; Prenylation; Lipoprotein.	
FT	NP_BIND_36 43 GTP (BY SIMILARITY).	
FT	NP_BIND_83 87 GTP (BY SIMILARITY).	
FT	NP_BIND_142 145 GTP (BY SIMILARITY).	
FT	NP_BIND_58 66 EFFECTOR_REGION (BY SIMILARITY).	
FT	LIPID_215 215 GERANYL-GERANYL (BY SIMILARITY).	
SEQUENCE	SEQUENCE 218 AA: 23764 MW; CID32CE7904322E5 CRC64;	
Query Match	30.0% Score 6 DB 1; Length 218:	
Best Local Similarity	100.0%; Pred. No. 21;	
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	8 PRGGGP 13	
DB	14 PRGGGG 19	
RESULT	13	
ASPx_HUMAN	ID ASPx_HUMAN STANDARD; PRT; 265 AA.	
AC	P26436; DR	
DT	01-AUG-1992 (Rel. 23, Created)	
DT	01-FEB-1996 (Rel. 33, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Acrosomal protein SP-10 precursor (Acrosomal vesicle protein-1).	
GN	OS	
OC	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1] NCBI_TaxID=9606;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RX	MEDLINE#90268085; PubMed=1693291;	
RA	Wright, R.M., John E., Klotz K., Flickinger C.J., Herr J.C.;	
RA	"Cloning and sequencing of cDNAs coding for the human intra-acrosomal antigen SP-10.", Biol. Reprod. 42:693-701(1990).	
RP	[2] REVISIONS.	
RA	Wright, R.M., John E., Klotz K., Flickinger C.J., Herr J.C., Biol. Reprod. 43:903-903(1990).	
RL	REPEAT	
RN	[3] SEQUENCE FROM N.A.	
RF	SEQUENCE FROM N.A.	
RX	MEDLINE#93385341; PubMed=8373955;	
RA	Wright, R.M., Suri, A.K., Kornreich, B., Flickinger C.J., Herr J.C.;	
RT	"Cloning and characterization of the gene coding for the human acrosomal protein SP-10.",	
FT	RL	
RN	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
RN	[5]	
RP	ALTERNATIVE SPlicing.	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RX	MEDLINE=9534748; PubMed=7619499;	
RA	Freemerman, A.J., Flickinger, C.J., Herr, J.C.;	
RA	"Characterization of alternatively spliced human SP-10 mRNAs.", Mol. Reprod. Dev. 41:100-108(1995).	
RN	[6]	
RP	SEQUENCE OF 78-100, 106-122 AND 127-151.	
RX	MEDLINE=92347498; PubMed=1637938;	
RA	Herr, J.C., Klotz, K., Shannon, J., Wright, R.M., Flickinger, C.J.;	
RA	Purification and microsequencing of the intra-acrosomal protein SP-10. Evidence that SP-10 heterogeneity results from endoproteolytic processes. ".	
RL	Biol. Reprod. 47:11-20(1992).	
CC	-!- SUBCELLULAR LOCATION: NASCENT ACROSOMAL VESICLE OF GOLGI PHASE SPERMATICS.	
CC	-!- ALTERNATIVE PRODUCTS: At least 11 isoforms; 1 (shown here), 2, 3, 4, 5, 6, 7, 8, 9, 10 and 11; are produced by alternative splicing.	
CC	-!- TISSUE SPECIFICITY: TESTIS.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; M82967; AAH36625; 1; -.	
DR	EMBL; M82968; AAH36626; 1; -.	
DR	EMBL; S65583; AAB28238; 2; -.	
DR	EMBL; S65606; AAB28238; 2; JOINED.	
DR	EMBL; S65576; AAB28238; 2; JOINED.	
DR	EMBL; S65578; AAB28238; 2; JOINED.	
DR	EMBL; BC014588; AAH11588; 1; -.	
DR	PIR; A37225; A37225.	
DR	Genew; HGNC:127; ACRV1.	
DR	MIM: 102525; -.	
KW	Signal; Glycoprotein; Repeat; Sperm; Alternative splicing.	
FT	SIGNAL_1 21 POTENTIAL.	
FT	CHAIN_22 265 ACROSOMAL PROTEIN SP-10.	
FT	DOMAIN_66 95 3 X 5 AA REPEATS OF S-E-H-[GA]-S.	
FT	REPEAT_66 70 1-1.	
FT	REPEAT_71 75 1-2.	
FT	REPEAT_91 95 1-3.	
FT	DOMAIN_85 168 4 X 4 AA REPEATS OF S-G-E-H.	
FT	REPEAT_85 88 2-1.	
FT	REPEAT_120 123 2-2.	
FT	REPEAT_145 148 2-3.	
FT	REPEAT_165 168 2-4.	
FT	DOMAIN_110 174 9 X 5 AA REPEATS OF [SV]-G-E-Q-[PSA].	
FT	REPEAT_110 114 3-1.	
FT	REPEAT_115 119 3-2.	
FT	REPEAT_125 129 3-3.	
FT	REPEAT_135 139 3-4.	
FT	REPEAT_140 144 3-5.	
FT	REPEAT_150 154 3-6.	
FT	REPEAT_155 159 3-7.	
FT	REPEAT_160 164 3-8.	
FT	REPEAT_170 174 3-9.	
FT	CARBHYD_258 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	VARSPLIC_41 95 MISSING (IN ISOFORM 3 AND ISOFORM 7).	
FT	VARSPLIC_41 110 MISSING (IN ISOFORM 4, ISOFORM 5, ISOFORM 8 AND ISOFORM 9).	
FT	VARSPLIC_41 135 MISSING (IN ISOFORM 6).	
FT	VARSPLIC_41 184 MISSING (IN ISOFORM 10).	

Run on: January 7, 2003, 12:37:29 ; Search time 11.7949 Seconds
 OM protein - protein search, using sw model

Title:	US-09-876-204-3
Perfect score:	20
Sequence:	MDGSEOPRGGPSSSEQIM 20
Scoring table:	OLIGO
Gapop:	60.0 , Gapext 60.0
Searched:	262574 seqs, 29422922 residues
Word size :	0

total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 3: /cgn2_6/pctodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/pctodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/pctodata/1/iaa/PCTUS.COMB.pep:*
- 6: /cgn2_6/pctodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	20	100.0	20	4 US-09-166-028-3
2	20	100.0	192	1 US-08-112-208C-2
3	20	100.0	192	1 US-08-112-208C-9
4	20	100.0	192	1 US-08-248-819A-2
5	20	100.0	192	1 US-08-248-819A-9
6	20	100.0	192	1 US-08-248-819A-9
7	20	100.0	192	1 US-08-471-058-13
8	20	100.0	192	2 US-08-337-646A-2
9	20	100.0	192	2 US-08-337-646A-9
10	20	100.0	192	2 US-08-856-531-2
11	20	100.0	192	2 US-08-856-531-9
12	20	100.0	192	2 US-08-856-534-2
13	20	100.0	192	2 US-08-856-534-9
14	20	100.0	192	3 US-08-471-057-13
15	20	100.0	192	4 US-09-127-048-7
16	20	100.0	192	4 US-08-927-326-2
17	20	100.0	192	4 US-08-927-326-9
18	20	100.0	192	5 PCT-US95-04600-25
19	20	100.0	221	1 US-08-616-732A-9
20	20	100.0	221	4 US-09-037-742B-9
21	15	75.0	25	1 US-08-790-897-21
22	15	75.0	25	2 US-08-978-523-21
23	11	55.0	20	4 US-09-166-08-5
24	11	55.0	41	1 US-08-112-208C-7
25	11	55.0	41	1 US-08-248-819A-7
26	11	55.0	41	2 US-08-337-646A-7
27	11	55.0	41	2 US-08-856-531-7

ALIGNMENTS

RESULT 1

US-09-166-028-3

; Sequence 3, Application US/09166028

; Patent No. 624585

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING REAGENTS AND METHODS

; TITLE OF INVENTION: REAGENTS AND METHODS

; FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09/166,028

; CURRENT FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 3

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-166-028-3

Query Match Best Local Similarity 100.0%; Score 20; DB 4; length 20; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Oy	1 MDGSEOPRGGPSSSEQIM 20
Db	1	MDGSEOPRGGPSSSEQIM 20

RESULT 2

US-08-112-208C-2

; Sequence 2, Application US/08112-208C

; Sequence 2, Application US/08112-208C-2

; Patent No. 5691179

; GENERAL INFORMATION:

; APPLICANT: KORMAYER, Stanley J.

; TITLE OF INVENTION: CELL DEATH REGULATORS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/112,208C

FILING DATE: 26-AUG-1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30.223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-112-208C-2

Query Match 100.0%; Score 20; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-08-112-208C-9
 Sequence 9, Application US/08112208C
 Patent No. 5691179
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248.819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30.223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-248-819A-2

Query Match 100.0%; Score 20; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-08-248-819A-2
 Sequence 2, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248.819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30.223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-248-819A-9

Query Match 100.0%; Score 20; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-08-248-819A-9
 Sequence 9, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/248,819A

FILING DATE: 25-NOV-1994

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/112,208

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-248-819A-9

Query Match 100.0%; Score 20; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGGPTSSQIM 20
 Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 6
 US-08-607-269-25
 Sequence 25, Application US/08607269
 ; Patent No. 570897

GENERAL INFORMATION:

APPLICANT: Reed, John C.

TITLE OF INVENTION: Interaction of Proteins Involved in a

TITLE OF INVENTION: Cell Death Pathway

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,058

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/320,157

FILING DATE: 07-OCT-1994

APPLICATION NUMBER: 08/110,067

FILING DATE: 30-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20007.12

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: 415-494-0792

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

US-08-607-269-25

Query Match 100.0%; Score 20; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Mismatches 0;
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGGPTSSQIM 20
 Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 8

US-08-337-646A-2

Sequence 2, Application US/08337646A

; Patent No. 585671

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/337,646A
 FILING DATE: 10-NOV-1994

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 25-MAY-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,819
 FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000620

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-337-646A-2

Query Match 100.0%; Score 20; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Length 192;
 Qy 1 MDGSGEQPRGGGPTTSEQM 20
 Db 1 MDGSGEQPRGGGPTTSEQM 20

RESULT 9
 US-08-337-646A-9

Sequence 9 Application US/08337646A
 ; Sequence 9 Application US/08337646A
 ; Patent No. 594290
 ; GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/856,531
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, Donald R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976176

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-337-646A-2

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,819
 FILING DATE: 25-MAY-1994

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000620

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-337-646A-9

Query Match 100.0%; Score 20; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Length 192;
 Qy 1 MDGSGEQPRGGGPTTSEQM 20
 Db 1 MDGSGEQPRGGGPTTSEQM 20

RESULT 10
 US-08-856-531-2

Sequence 2 Application US/080856531
 ; Sequence 2 Application US/080856531
 ; Patent No. 594290
 ; GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howell & Haferkamp, L.C.
 STREET: 7733 Forsyth Blvd., Suite 1400
 CITY: St. Louis
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/856,531
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, Donald R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976176

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856 531-2

Query Match 100 %; Score 20; DB 2; Length 192;

Best Local Similarity 100 %; Pred. No. 1.5e-12; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQOPRGGGPSSSEQIM 20

Db 1 MDGSGEQOPRGGGPSSSEQIM 20

RESULT 11
US-08-856 531-9
Sequence 9, Application US/08856531

; Patent No. 5942490

GENERAL INFORMATION:
APPLICANT: KORMMEYER, Stanley J.TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31CORRESPONDENCE ADDRESS:
STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856, 034

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188

TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-034-2

Query Match 100 %; Score 20; DB 2; Length 192;

Best Local Similarity 100 %; Pred. No. 1.5e-12; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQOPRGGGPSSSEQIM 20

Db 1 MDGSGEQOPRGGGPSSSEQIM 20

RESULT 12
US-08-856-034-2
Sequence 2, Application US/08856034

; Patent No. 5955595

GENERAL INFORMATION:

APPLICANT: KORMMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31CORRESPONDENCE ADDRESS:
STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856, 034

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188

TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION: /note= "Human BAX polypeptide"

GenCore version 5.1.3
copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on : January 7, 2003, 12:31:28 ; Search time 31.7949 Seconds
(without alignments)
83.819 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20 ; Sequence: 1 MDGSGEQPRGGPPTTSEQIM 20

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/

ALIGNMENTS

RESULT 1

ID AAY90736 standard; peptide: 20 AA.

ID AAY90736;

DT 17-AUG-2000 (first entry)

DE Human BAX amino acid sequence 1 to 20 SEQ ID NO:2.

XX Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;

KW cell death; cancer; cytostatic.

OS Homo sapiens.

XX WO200020446-A2.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-1B01680.

PR 05-OCT-1998; 98US-0166028.

PA (UVMC-) UNIV MCGILL.

XX PI Shore GC, Goping S;

XX DR WPI; 2000-303740/26.

XX PT BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer.

XX PS Example 2; Page 52; 53pp; English.

A human Bcl-2 asso

Human BAX amino acid sequence: Amino acid sequence Human bcl-2 associ Human Bax protein. Human Bax. Homo s Human Bax protein. Human Bax polypept Human Bax omega protein, Truncated Bax amin Coding region of c Rat BAX amino acid A Bcl-2 associated N-terminus of Baxg Mouse BAX amino ac Mouse BAX neuroprotect Mouse Bax proteo

Mouse Bcl-2 assoc Mouse neuroprotect Mouse neuroprotect. Murine Bcl-2 assoc Murine Bax protein Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Murine Bcl-2 assoc Murine BAX alpha pr Murine bcl-2 assoc Murine bcl-2 assoc Murine Bax. Murine Bax polypep Apoptotic regulati Human protein SEO Human protein SEO Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

The present invention describes a pure protein (P1) comprising a BAX polypeptide lacking an apoptotic regulation or targeting (ART) domain. CC P1 has cytostatic activity and can be used in the modulation of CC apoptosis. The polypeptides and methods from the present invention are CC useful for identifying compounds that modulate apoptosis which can then CC be used for treating cancer. The present sequence represents a human BAX peptide sequence of amino acids 1 to 20, which is used in an CC example from the present invention.

SQ Sequence 20 AA;

Match	Score	DB	Length	20;
Best Local Similarity	100.0%	21;	Length	20;
Matches	100.0%	Pred.	No.	1.8e-12;
20;	conservative	0;	Mismatches	0;
Ov	1	Indels	0;	Gaps
Db	1	MDGSGEOPRGGGPNSSEQM	20	
			
		MDGSGEOPRGGGPNSSEQM	20	

RESULT 2

ID	AAV70816 standard; Protein; 70 AA.	
XX		
AC	AAY70816;	
DT	31-JUL-2000 (first entry)	
DE	Human neuroprotective truncated BAX protein, tBAX70.	
KW	Human; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family; neuron; anti-apoptotic; cerebroproTECTive; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.	
KW		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..58
FT	Domain	/notes "N-terminal region of BAX alpha"
FT		59..70
FT		/label= Partial BH3 domain
FT		/note= "BH3 domain in the full-length BAX alpha consists of amino acids 59-73"
PN	W020023083-A1.	
XX		
PD	27-APR-2000.	
XX		
PF	22-OCT-1999; 99WO-US24747.	
PR	22-OCT-1998; 98US-0177315.	
XX		
PA	(UNIV) UNIV WASHINGTON.	
XX		
XX	Johnson EM, Easton R;	
PI		
XX	DR WPI; 2000-339513/29.	
XX		
PT	Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -	
XX		
PS	Claim 4; Page 32; 43PP; English.	
XX		
CC	The present sequence is a specifically claimed truncated BAX protein	
CC	TBAx70 which inhibits neuronal apoptosis induced by trophic factor	
CC	deprivation. The protein consists of first 70 amino acids of human	
CC	BAX alpha, that includes the N-terminal region and a portion of the BH3	
CC	domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of	
CC	the full-length BAX alpha. The TBAx protein lacking only the	
CC	transmembrane domain has been shown to have anti-apoptotic activity.	
CC	The present sequence is used to treat diseases associated with neuronal	

XX
Sequence 70 AA:
SQ

	Db	1 MDGSGEOPRGGGPTSSEQIM 20
Query Match	100.0%	Score 20; DB 21; Length 70;
Best Local Similarity	100.0%	Pred. No. 5.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches	20;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MDGSGEOPRGGGPTSSEQIM 20	
Db	1 MDGSGEOPRGGGPTSSSEQIM 20	

RESULT 4
AAY70818
ID AAY70818 standard; Protein; 78 AA.
XX
AC AAY70818;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human neuroprotective truncated BAX protein, tBAX78.
XX
Homo sapiens.
OS Synthetic.

XX
FH Human; truncated BAX protein; tBAX78; BAX alpha; Bcl-2 family; mutant; neuron; anti-apoptotic; cerebroprotection; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.

XX
KW Human; truncated BAX protein; tBAX78M; BAX alpha; Bcl-2 family; mutant; neuron; anti-apoptotic; cerebroprotection; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.

XX
PR 1..58 /note= "N-terminal region of BAX alpha"
FT 59..73 /label= BH3_domain

XX
PN WO20023083-A1.
XX
PD 27-APR-2000.
XX
PF 22-OCT-1999; 99WO-US24747.
XX
PR 22-OCT-1998; 98US-0177315.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Johnson EM, Easton R;
XX
DR WPI; 2000-339513/29.
DR N-FSDB; AAD00125.
XX
PT Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
XX
PS Claim 4; Page 33; 43pp; English.

XX
PT Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
XX
PS Claim 4; Page 34; 43pp; English.

CC The present sequence is a specifically claimed truncated BAX protein, CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by CC trophic factor deprivation. The protein consists of the N-terminal CC region and a portion of BH3 domain of human BAX alpha, and a novel CC C-terminal sequence of 8 amino acids not present in BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the CC transmembrane domain has been shown to have anti-apoptotic activity. CC The present sequence is used to treat diseases associated with neuronal CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.

XX
SQ Sequence 78 AA:
Query Match 100.0% Score 20; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.8e-12; Mismatches 0; Indels 0; Gaps 0;

	Db	1 MDGSGEOPRGGGPTSSSEQIM 20
Query Match	100.0%; Score 20; DB 21; Length 78;	
Best Local Similarity	100.0%; Pred. No. 5.8e-12; Mismatches 0; Indels 0; Gaps 0;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDGSGEOPRGGGPTSSSEQIM 20	
Db	1 MDGSGEOPRGGGPTSSSEQIM 20	

RESULT 5
AAY70822
ID AAY70822 standard; Protein; 78 AA.
XX
AC AAY70822;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human neuroprotective truncated BAX protein tBAX78 mutant.
XX
KW Human; truncated BAX protein; tBAX78M; BAX alpha; Bcl-2 family; mutant; neuron; anti-apoptotic; cerebroprotection; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.

XX
PR 1..58 /note= "Wild type Ser is substituted by Ala"
FT 59..73 /label= BH3_domain

XX
PN WO20023083-A1.
XX
PD 27-APR-2000.
XX
PF 22-OCT-1999; 99WO-US24747.
XX
PR 22-OCT-1998; 98US-0177315.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Johnson EM, Easton R;
XX
DR WPI; 2000-339513/29.
DR N-FSDB; AAD00125.

XX
PT Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
XX
PS Claim 4; Page 34; 43pp; English.

CC The present sequence is a specifically claimed truncated BAX protein, CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by CC trophic factor deprivation. The protein consists of the N-terminal CC region and a portion of BH3 domain of human BAX alpha, and a novel CC C-terminal sequence of 8 amino acids not present in BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the CC transmembrane domain has been shown to have anti-apoptotic activity. CC The present sequence is used to treat diseases associated with neuronal CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.

XX
SQ Sequence 78 AA:
Query Match 100.0% Score 20; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.8e-12; Mismatches 0; Indels 0; Gaps 0;

AAV34149
ID AAV34149 standard; Protein; 131 AA.
XX
AC AAV34149;
XX
DT 30-NOV-1999 (first entry)
DE Human truncated Bax protein.
XX
KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
XX
OS Homo sapiens.
XX
Key location/Qualifiers
FH 59..101
FT /notes "Portion of BH3 domain essential for dimerisation"
XX
PN WO9946371-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05359.
XX
PR 11-MAR-1998; 98US-0077541.
XX
(TEXA) UNIV TEXAS SYSTEM.
XX
PT McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
PI Ji L, Roth JA;
XX
DR WPI; 1999-551404/46.
DR N-PSDB; AAZ19763.
XX
PS New adenovirus vectors, used for killing or inhibiting the growth of
PT cells and for treating cancers
XX
Claim 26; Page 148-149; 151pp; English.
XX
CC This sequence represents a human truncated Bax protein. The cDNA
CC contains a single base deletion relative to the wild-type (AAZ19764),
CC causing a frameshift which leads to translation of a premature stop
CC codon, resulting in a truncated protein. However, the domain responsible
CC for its function is still present in the truncated protein. Bax (Bcl-2
CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
CC Bax functions as a primary response gene in the p53-regulated apoptotic
CC pathway. The Bax gene promoter has 4 p53 binding sites and the
CC expression of Bax is upregulated at the transcriptional level by p53, and
CC Bax mRNA and protein expression have been shown to increase following
CC induction of p53. Bax protein can function as a homodimer, or it can
CC heterodimerise with other Bcl-2 gene family members such as the
CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
CC provides a means of controlling cell death via the "rheostat" model. This
CC model suggests that the relative amounts of Bcl-2 and Bax determine the
CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
CC in excess, however, Bax homodimers predominate and the cell becomes
CC susceptible to apoptosis following exposure to a apoptotic stimulus.
CC Additionally, Bax can function in its monomeric form to accelerate cell
CC death. Use of novel adenoviral vectors containing this Bax gene may
CC augment and complement wild-type p53 gene therapy, which induces a G1
CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
CC mutations. In addition, Bax overexpression could provide the apoptotic
CC effect of p53 without the need for p53 itself.
XX
Sequence 131 AA;

Query Match 100.0%; Score 20; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.1e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGHQPRGGPPTSBOIM 20
Db 1 MDGSGHQPRGGPPTSSEQIM 20

RESULT 7
ID AAR71406
ID AAR71406 standard; Protein; 192 AA.
XX
AC AAR71406;
XX
DE Human Bax protein.
XX
KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
KW proliferation; cell cycle progression; Bax; apoptotic cell death;
KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
KW ischaemic cell death.
XX
OS Homo sapiens.
XX
PN WO9505750-A.
XX
PD 02-MAR-1995.
XX
PR 24-AUG-1994; 94WO-US09701.
XX
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Kormeyer SJ;
XX
DR WPI; 1995-106605/14.
DR N-PSDB; AAQ97606.

XX
PT Methods for producing and identifying mutant bcl-2 proteins -
PT that lack death repressor activity and/or lacks binding to Bax.
XX
PS Disclosure; Fig 3; 133pp; English.

XX
CC This sequence represents human Bax protein. Bax is a protein which is
CC associated with the human bcl-2 alpha and beta proteins, the sequences
CC of which are given in AAR71404-05 respectively. bcl-2 is encoded by a
CC proto-oncogene and is capable of inhibiting apoptosis in many
CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
CC cytoplasmic protein and is thought to function by enhancing the survival
CC of hematopoietic cells of B and T origins rather than directly promoting
CC proliferation of these cell types. bcl-2 has not been shown to directly
CC promote cell cycle progression nor does it necessarily alter the dose
CC response to limiting concentrations of IL-3. bcl-2 has been shown to
CC form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
CC accelerates apoptotic cell death induced by cytokine deprivation in an
CC IL-3 dependent cell line, and it also acts to counter the death repressor
CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
CC cell survival or death following an apoptotic stimulus. The invention
CC gives a mutant form of bcl-2 in which there is at least one amino acid
CC substitution or deletion in the BH1 or BH2 domains. This makes the
CC mutant protein substantially incapable of binding Bax and/or incapable
CC of death repressor activity. Down regulation of bcl-2 is useful in
CC cancer therapy, controlling hyperplasias and eliminating self-reactive
CC clones in autoimmunity by favouring death effector molecules. Up
CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
CC cell death.

XX
SQ Sequence 192 AA;

Query Match 100.0%; Score 20; DB 16; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGGPTSSSEQIM 20
 ||||||| ||||| ||||| |||||
 ID AAY34150 standard; Protein: 192 AA.
 1 MDGSGEOPRGGGPTSSSEQIM 20

RESULT 8
 AAY34150
 ID AAY34150 standard; Protein: 192 AA.
 AC AAY34150;
 XX
 30-NOV-1999 (first entry)
 XX
 DE Human wild-type Bax protein.
 KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 59..101 /note= "portion of BH3 domain essential for dimerisation"
 XX
 W09946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077341.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 JI L, Roth JA;
 DR WPI; 1999-551404/46.
 XX
 DR-PSDB; AA219764.

XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers - disclosure; Page 149-150; 151pp; English.
 XX
 PS This sequence represents human wild-type Bax protein. A naturally occurring mutant protein (AY34149) was also isolated. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the expression of Bax is upregulated at the transcriptional level by p53, and induction of p53. Bax protein can function as a homodimer, or it can heterodimerise with other Bcl-2 gene family members such as the antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members provides a means of controlling cell death via the "rheostat" model. This model suggests that the relative amounts of Bcl-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing the Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.

XX Sequence 192 AA;

QY 1 MDGSGEOPRGGGPTSSSEQIM 20
 ||||||| ||||| ||||| |||||
 ID AAY05435 standard; peptide: 192 AA.
 1 MDGSGEOPRGGGPTSSSEQIM 20

RESULT 9
 AAY05435
 ID AAY05435 standard; peptide: 192 AA.
 XX
 AC AAY05435;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX protein sequence.
 KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.
 KW Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 PN W09916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 22-SEP-1998; 98WO-US19765.
 XX
 PR 07-OCT-1997; 97US-0946039.
 XX
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 DR WPI; 1999-255058/21.
 XX
 PT Bcl homology domain 3 polypeptide
 XX
 PS Disclosure; Fig 21c; 104pp; English.
 CC This sequence represents the human BAX protein.
 CC The invention relates to a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell, a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death regulation.
 CC Sequence 192 AA;

Query Match 100.0%; Score 20; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGGPTSSSEQIM 20
 ID AAY05435 standard; peptide: 192 AA.
 1 MDGSGEOPRGGGPTSSSEQIM 20

RESULT 10
 AAW87804 standard; Protein: 192 AA.
 XX
 AC AAW87804;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE A human Bcl-2 associated protein designated Bax.
 XX

Query Match 100.0%; Score 20; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
bcl-2-related function; apoptosis.
XX
OS Homo sapiens.
XX
FH
Key
Domain Location/Qualifiers
97..118
/note= "BHL domain"
146..168
/note= "BH2 domain"
XX
PN US5856171-A.
XX
PD 05-JAN-1999.
XX
PF 10-NOV-1994; 94US-0337646.
XX
PR 10-NOV-1994; 94US-0337646.
XX
CC 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PT Korsmeyer SJ;
XX
DR WPI; 1999-105119/09.
DR N-PSDB; AAV84005.
XX
PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
PT identifying modulators of bcl-2 function
XX
PS Example 1; Columns 71-74; 105pp; English.
XX
XN The present sequence represents a human Bcl-2 associated protein
CC designated Bax. The Bax protein is used in a composition which
CC comprises a bcl-2 family member polypeptide, a naturally occurring
CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
CC The composition is used to identify modulators of bcl-2-related
CC function, e.g. substances that inhibit binding of Bax to bcl-2,
CC which would be potentially useful as drugs for modulating
CC apoptosis.
XX
SQ Sequence 192 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	20	192
Matches	100.0%	Pred. No.	1.3e-11
	0	Mismatches	0
	0	Indels	0
	0	Gaps	0

Qy 1 MDGSGEOPRGGGPTSSEQIM 20
Db 1 MDGSGEOPRGGGPTSSEQIM 20
RESULT 12
AYY70827
ID AYY70827 standard; Protein: 192 AA.
XX
AC AYY70827;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human BAX alpha protein.
XX
HU Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
XX
OS Homo sapiens.
XX
FH
Key
Region Location/Qualifiers
1..58
/label= N-terminal_region
FT Domain
59..73
/label= BH3_domain
FT
DT 10-MAR-1999 (first entry)
XX
A human Bcl-2 associated protein designated Bax.
XX
KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KW bcl-2-related function; apoptosis.
XX
OS Homo sapiens.
XX
PN US5856171-A.
XX
PD 05-JAN-1999.
XX
PR 10-NOV-1994; 94US-0337646.
XX
PT Korsmeyer SJ;
XX
DR WPI; 1999-105119/09.
XX
PS Example 7; Fig 7; 105pp; English.
XX
CC The present sequence represents a human Bcl-2 associated protein
CC designated Bax. The Bax protein is used in a composition which
CC comprises a bcl-2 family member polypeptide, a naturally occurring
CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
CC The composition is used to identify modulators of bcl-2-related
CC function, e.g. substances that inhibit binding of Bax to bcl-2,
CC which would be potentially useful as drugs for modulating
CC apoptosis.
XX
SQ Sequence 192 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	20	192
Matches	100.0%	Pred. No.	1.3e-11
	0	Mismatches	0
	0	Indels	0
	0	Gaps	0

Qy 1 MDGSGEOPRGGGPTSSEQIM 20
Db 1 MDGSGEOPRGGGPTSSEQIM 20
RESULT 12
AYY70827
ID AYY70827 standard; Protein: 192 AA.
XX
AC AYY70827;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human BAX alpha protein.
XX
HU Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
XX
OS Homo sapiens.
XX
FH
Key
Region Location/Qualifiers
1..58
/label= N-terminal_region
FT Domain
59..73
/label= BH3_domain
FT
FT Domain
98..118
/label= BHL_domain
150..165
FT Domain
169..188
/label= BH2_domain
169..188
/label= Transmembrane_domain
XX
PN WO200023083-A1.
XX
PD 27-APR-2000.
XX
PR 22-OCT-1999; 99WO-US24747.
XX
PT 22-Oct-1998; 98US-0177315.

XX
PA (UNIW) UNIV WASHINGTON.
XX
PI XX
XX Johnson EM, Estton R;
DR
WPI; 2000-339513/29.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
PS Disclosure; Page 35-36; 43pp; English.
XX
CC The present sequence is a human BAX alpha protein, a pro-apoptotic
protein which is a member of BCL-2 family of proteins that are involved
in regulation of neuronal programmed cell death. The patent discloses
specific truncated proteins derived from BAX alpha which inhibit neuronal
apoptosis induced by trophic factor deprivation.
CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
CC These proteins contain the N-terminal region and at least a portion of
the BH3 domain of BAX alpha and lack the BHL, BH2 and C-terminal
transmembrane domains. The tBAX protein lacking only the
CC spinal cord injury, head trauma and stroke.
CC The tBAX proteins are used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC XX

SQ sequence 192 AA:
Query Match 100.0%; Score 20; DB 21; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSGEOPRGGPSSEQIM 20
Db 1 MDGSGEOPRGGPSSEQIM 20

RESULT 13
AY69302
TD AAY69302 standard; peptide; 192 AA.
XX
AC AAY69302;
XX
DT 30-MAY-2000 (first entry)
DE Amino acid sequence of the human Bax protein.
XX
KW pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;
cytochrome C transport; mitochondria; apoptosis; ion selectivity;
anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus;
African swine fever virus; adenovirus; lymphoproliferative condition;
cancer; arthritis; Crohn's disease; inflammation; autoimmune disease;
immunodeficiency; senescence; neurodegenerative disease;
repertusory cell death; infertility; wound.
XX
OS Homo sapiens.
XX
PN WO200006187-A2.
XX
PR 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-US17276.
XX
PR 31-JUL-1998; 98US-0127048.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ, Schlesinger PH;
XX
WPI; 2000-195193/17.

PT Modulating apoptosis in cells by modulating channel ion selectivity for
transport of cytochrome C -

XX
PS Disclosure; Page 34; 57pp; English.
XX
CC The present sequence represents the Bax protein. A pro-apoptotic
peptide can be derived from the BH3 domain. The peptide is an inducer
of formation of a channel for transport of cytochrome C out of
mitochondria. The peptide induces apoptosis in a cell. The peptide
changes the ion selectivity of an anti-apoptotic BCL-2 family member
from potassium selective to chloride selective. The specification
also describes inhibitors of apoptosis in cells. The inhibitors and
inducers can be used to treat patients, preferably humans with a
condition mediated by excessive down-regulation of apoptosis,
especially conditions chosen from neoplasias, diseases caused by
Epstein Barr virus, African swine fever virus and adenovirus,
lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
inflammation and autoimmune disease or a condition mediated by
excessive apoptosis, especially immunodeficiency diseases, senescence,
neurodegenerative disease, ischemic and reperfusion cell death,
fertility and wounds. The methods can also be used to identify
apoptosis-modulating compounds.

XX
SQ Sequence 192 AA:
Query Match 100.0%; Score 20; DB 21; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSGEOPRGGPSSEQIM 20
Db 1 MDGSGEOPRGGPSSEQIM 20

RESULT 14
AAB74121
ID AAB74121 standard; Protein; 192 AA.
XX
AC AAB74121;
XX
DT 22-MAY-2001 (first entry)
DE Human bcl-2 associated X protein (Bax) #1.
XX
Human; Bax; Cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischaemia;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.
XX
OS Homo sapiens.
XX
PN US6184202-B1.
XX
PD 06-FEB-2001.
XX
PF 11-SEP-1997; 97US-0927326.
XX
PR 10-NOV-1994; 94US-0337646.
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 2001-256104/26.
DR N-PSDB; AAB77704.

XX
PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
adult tissues, or treating proliferative or autoimmune diseases,
PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
bcl-2 associated X protein -

PS	Claim 3; Fig 1; 105pp; English.
CC	The present invention relates to a method of modulating apoptosis of a cell. The method comprises administering to the cell an agent, comprising a BHL domain or BH2 domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially useful in cancer therapy, and treating autoimmunity, immunodeficiency diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke, traumatic brain injury, neurodegenerative diseases, aging, ischaemia, toxæmia, infection, hepatitis, transplant rejection, and lymphoproliferative diseases. The present sequence is human Bax, which was used in the method of the present invention.
CC	SQ Sequence 192 AA;
CC	Query Match 100.0%; Score 20; DB 22; Length 192;
CC	Best Local Similarity 100.0%; Pred. No. 1.3e-11; Mismatches 0; Indels 0; Gaps 0
CC	Matches 20; Conservative 0; QY 1 MDGSQEOPRGGGTTSSEQIM 20
CC	Db 1 MDGSQEOPRGGGTTSSEQIM 20
XX	RESULT 15
XX	AAB74126
XX	ID AAB74126 standard; Protein: 192 AA.
XX	AC AAB74126;
XX	DT 22-MAY-2001 (first entry)
XX	DE Human bcl-2 associated X protein (Bax) #2.
XX	KW Human; Bax; cytostatic; immunosuppressive; immunostimulant; infection; apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS; autoimmunity; immunodeficiency; reperfusion injury; stroke; aging; myocardial infarction; traumatic brain injury; ischaemia; neurodegenerative diseases; hepatitis; transplant rejection; toxæmia; lymphoproliferative disease.
XX	OS Homo sapiens.
XX	PN US6184202-B1.
XX	PD 06-FEB-2001.
XX	PP 11-SEP-1997; 97US-0927326.
PR	10-NOV-1994; 94US-0337646.
PR	26-AUG-1993; 93US-0112208.
PR	25-MAY-1994; 94US-0248819.
XX	(UNIW) UNIV WASHINGTON.
PA	PI Korsmeyer SJ;
XX	DR WPI; 2001-256104/26.
XX	Modulating apoptosis of a cell, useful in maintaining homeostasis in adult tissues, or treating proliferative or autoimmune diseases, bcl-2 associated X protein - comprises administering a bcl-2 polypeptide that interacts with a 21 kD bcl-2 associated X protein -
PS	Example 7; Fig 7; 105pp; English.
CC	The present invention relates to a method of modulating apoptosis of a cell. The method comprises administering to the cell an agent, comprising a BHL domain or BH2 domain, capable of modulating formation of at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax

REFERENCE/DOCKET NUMBER: 976175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Murine BAX polypeptide"
 US-08-856-034-3

Query Match 88.5%; Score 69; DB 2; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MDGSGXXXXGGPTSSBQI 19
 Db 1 MDGSGPOLGSGGPTSSBQI 19

RESULT 11
 US-08-856-034-8
 Sequence 8, Application US/08856034
 ; Patent No. 5355595
 GENERAL INFORMATION:
 APPLICANT: KORMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howell & Haferkamp, L.C.
 STREET: 7733 Forsyth Blvd., Suite 1400
 CITY: St. Louis
 STATE: MO
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/856,034
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, Donald R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Murine BAX polypeptide"
 US-08-856-034-8

Query Match 88.5%; Score 69; DB 2; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05; Indels 5; Mismatches 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 12
 US-09-127-048-6
 Sequence 6, Application US/09127048
 ; Patent No. 6165132
 GENERAL INFORMATION:
 APPLICANT: KORMEYER, Stanley J.
 TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
 CURRENT APPLICATION NUMBER: US/09/127,048
 CURRENT FILING DATE: 1/98-07-31
 EARLIER FILING DATE: 6/01-06/1,823
 EARLIER FILING DATE: 1997-10-14
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 6
 LENGTH: 192
 TYPE: PRT
 ORGANISM: Mouse
 US-09-127-048-6

Query Match 88.5%; Score 69; DB 4; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MDGSGXXXXGGPTSSBQI 19
 Db 1 MDGSGEOLGGGGPTSSBQI 19

RESULT 13
 US-08-927-326-3
 Sequence 3, Application US/08927326
 ; Patent No. 6184202
 GENERAL INFORMATION:
 APPLICANT: KORMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 3739 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,326
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000620
 TELECOMMUNICATION INFORMATION:

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:IAS MBP 90-101
 OTHER INFORMATION: CHI.H.CH2 recombinant MHC class II-peptide-Ig
 OTHER INFORMATION: fusion complex
 US-09-815-837-70

Query Match 46.2%; Score 36; DB 10; Length 562;
 Best Local Similarity 53.3%; Pred. No. 81; Mismatches 6; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GSGXXXXXXGPPSE 17
 ||| :|||
 Db 243 GGGGGGGGGSSSE 257

RESULT 14
 US-09-815-837-69
 Sequence 69, Application US/09815837
 Patent No. US20020082411A1

GENERAL INFORMATION:
 APPLICANT: Carter, Darrick
 APPLICANT: Zhu, Shirley
 APPLICANT: Arimilli, Subhashini
 APPLICANT: Wang, Aijun
 APPLICANT: Corixa Corporation

TITLE OF INVENTION: Immune Mediators and Related Methods
 FILE REFERENCE: 014058-005670US

CURRENT APPLICATION NUMBER: US/09/815, 837

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 60/191, 274

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: US 60/204, 249

PRIOR FILING DATE: 2000-05-15

PRIOR APPLICATION NUMBER: US 60/264, 003

PRIOR FILING DATE: 2001-01-23

NUMBER OF SEQ ID NOS: 129

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 69

LENGTH: 676

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:IAS-MBP 1-14
 OTHER INFORMATION: CH1.H recombinant MHC class II-peptide-Ig fusion
 OTHER INFORMATION: complex
 US-09-815-837-69

Query Match 46.2%; Score 36; DB 10; Length 678;
 Best Local Similarity 53.3%; Pred. No. 98; Mismatches 6; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GSGXXXXXXGPPSE 17
 ||| :|||
 Db 243 GGGGGGGGGSSSE 257

Search completed: January 7, 2003, 12:37:21
 Job time : 8.30769 secs

RESULT 15
 US-09-815-837-68
 Sequence 68, Application US/09815837
 Patent No. US20020082411A1

GENERAL INFORMATION:
 APPLICANT: Carter, Darrick
 APPLICANT: Zhu, Shirley
 APPLICANT: Arimilli, Subhashini
 APPLICANT: Wang, Aijun
 APPLICANT: Corixa Corporation

TITLE OF INVENTION: Immune Mediators and Related Methods
 FILE REFERENCE: 014058-005670US

CURRENT APPLICATION NUMBER: US/09/815, 837

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 60/191, 274

PRIOR FILING DATE: 2000-03-22



FILING DATE: 26-AUG-1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Protein sequence of murine
 OTHER INFORMATION: Bax."
 US-08-112-208C-3

Query Match 88.5%; Score 69; DB 1; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 5;
 Indels 0; Gaps 0;

RESULT 3
 US-08-112-208C-8
 Sequence 8, Application US/08112208C
 Patent No. 5691179
 GENERAL INFORMATION:
 APPLICANT: KORMSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,819A
 FILING DATE: 25-NAY-1994
 CLASSIFICATION: 535
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Protein sequence of murine
 OTHER INFORMATION: Bax."
 US-08-248-819A-3

Query Match 88.5%; Score 69; DB 1; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 5;
 Indels 0; Gaps 0;

RESULT 4
 US-08-248-819A-3
 Sequence 3, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 APPLICANT: KORMSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,819A
 FILING DATE: 25-NAY-1994
 CLASSIFICATION: 535
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,208
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Protein sequence of murine
 OTHER INFORMATION: Bax."
 US-08-248-819A-3

Query Match 88.5%; Score 69; DB 1; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 5;
 Indels 0; Gaps 0;

RESULT 5
 US-08-248-819A-8
 Sequence 8, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 APPLICANT: KORMSMAYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60

Query Match

88.5%; Score 69; DB 1; Length 192;

• 1

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-337-646A-8

Query Match 88.5%; Score 69; DB 2; Length 192;
 Best Local Similarity 73.7%; Pred. No. 3.2e-05; 0; Mismatches 5; Indels 0; Gaps 0;
 Matches 14; conservative

QY 1 MDGSGXXXXGGPSSSEQI 19
 ||||| |||||||
 Db 1 MDGSGEQLGSGGPSSSEQI 19

RESULT 8
 US-08-856-531-3

; Sequence 3, Application US/08856531
 ; Patient No. 594290
 ; GENERAL INFORMATION:
 ; APPLICANT: KORMSMAYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howell & Haferkamp, L.C.
 ; STREET: 7733 Forsyth Blvd., Suite 1400
 ; CITY: St. Louis
 ; STATE: MO
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: pc-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/856, 531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, Donald R.
 ; REGISTRATION NUMBER: 35, 197
 ; REFERENCE/DOCKET NUMBER: 976176
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 314-727-5188
 ; TELEFAX: 314-727-5002
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 192 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..192
 ; OTHER INFORMATION: /note= "Murine BAX polypeptide"
 ; US-08-856-531-8

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..192
 OTHER INFORMATION: /note= "Murine BAX polypeptide"
 ; US-08-856-531-3

RESULT 10
 US-08-855-034-3

; Sequence 3, Application US/08856034
 ; Patient No. 595595
 ; GENERAL INFORMATION:
 ; APPLICANT: KORMSMAYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howell & Haferkamp, L.C.
 ; STREET: 7733 Forsyth Blvd., Suite 1400
 ; CITY: St. Louis
 ; STATE: MO
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: pc-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/856, 034
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, Donald R.
 ; REGISTRATION NUMBER: 35, 197

RESULT 9
 US-08-856-531-8

; Sequence 8, Application US/08856531
 ; Patient No. 594290
 ; GENERAL INFORMATION:
 ; APPLICANT: KORMSMAYER, Stanley J.
 ; TITLE OF INVENTION: CELL DEATH REGULATORS

RESULT 13
 US-09-724-676A-82068
 ; Sequence 82068, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 82068
 ; LENGTH: 1054
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676A-82068

RESULT 14
 US-09-724-676-82069
 ; Sequence 82069, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 82069
 ; LENGTH: 1149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676-82069

Query Match 46.2%; Score 36; DB 5; Length 1054;
 Best Local Similarity 37.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 Qy 3 GSGXXXXXGGPTSEQ 18
 Db 237 GGGAAASSVGGPNGKQ 252

RESULT 15
 US-09-724-676A-82069
 ; Sequence 82069, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724,676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 82069
 ; LENGTH: 1149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676A-82069

Query Match 46.2%; Score 36; DB 5; Length 1149;
 Best Local Similarity 37.5%; Pred. No. 3e+02;
 Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy	3 GSGXXXXXGGPTSEQ 18
Db	237 GGGAAASSVGGPNGKQ 252

Search completed: January 7, 2003, 12:36:59
 Job time : 12.2051 secs

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 126
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-23-553-126

Query Match 47.4%; Score 37; DB 7; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GSGXXXGGPSS 17
Db 623 GGGGSGASGGPTIEE 637
Length: 299
US-60-427-579-126

Query Match 47.4%; Score 37; DB 7; Length 639;
Sequence 126, Application US/60427579
GENERAL INFORMATION:
APPLICANT: American Home Product Inc.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRESSIVE DISORDERS
FILE REFERENCE: AMI01250L
CURRENT APPLICATION NUMBER: US/60/427,579
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 256
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 126
LENGTH: 639
TYPE: PRT
ORGANISM: Homo sapiens
US-09-427-579-126

Query Match 47.4%; Score 37; DB 7; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GSGXXXGGPSS 17
Db 623 GGGGSGASGGPTIEE 637
Length: 299
US-09-134-000C-6041

Query Match 47.4%; Score 37; DB 7; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GSGXXXGGPSS 17
Db 623 GGGGSGASGGPTIEE 637
Length: 299
US-09-134-000C-6041

Query Match 47.4%; Score 37; DB 7; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GSGXXXGGPSS 17
Db 623 GGGGSGASGGPTIEE 637
Length: 299
US-09-134-000C-6041

Query Match 47.4%; Score 37; DB 5; Length 748;
Best Local Similarity 87.5%; Pred. No. 1.3e+02; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGTTTSEQ 18
Db 41 GGTTTSHQ 48
Length: 1054
US-09-724-676-82068

Query Match 46.2%; Score 36; DB 5; Length 1054;
Best Local Similarity 37.5%; Pred. No. 2.8e+02; 9; Mismatches 6; Indels 1; Gaps 0;
Matches 6; Conservative 1; Mismatches 9; Indels 1; Gaps 0;

QY 3 GSXXXXXGGPTTS 18

```

RESULT 10

; ORGANISM: Homo sapiens
US-10-306-878-5

Query Match 85.9%; Score 67; DB 6; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00015; 0; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDGSGXXXGGPISSEQI 19
Db 1 MDGSGXXXGGPISSEQI 19

RESULT 3
US-10-196-793A-46

; Sequence 45, Application US/10196793A

; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MARTIN G.
; TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS
; FILE REFERENCE: CLFR-0120S
; CURRENT APPLICATION NUMBER: US/10/196,793A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 60/360,361
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/332,886
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 46
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US 10-196-793A-46

Query Match 79.5%; Score 62; DB 6; Length 191;
Best Local Similarity 72.2%; Pred. No. 0.0012; 5; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGGGXXXXGGPISSEQI 19
Db 1 DGGGXXXXGGPISSEQI 18

RESULT 4
US-10-264-237-2133

; Sequence 233, Application US/10264237

; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2133
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 79.5%; Score 62; DB 6; Length 191;
Best Local Similarity 72.2%; Pred. No. 0.0012; 5; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGGGXXXXGGPISSEQI 19
Db 1 DGGGXXXXGGPISSEQI 18

RESULT 5
US-09-724-676-64483

; Sequence 6483, Application US/09724676

; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 91222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 64483
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-64483

Query Match 47.4%; Score 37; DB 5; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GSGXXXXGGPISSEQE 17
Db 623 GGGGSGASGGTIEE 637

RESULT 6
US-09-724-676A-64483

; Sequence 6483, Application US/09724676A

; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 91222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 64483
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-64483

Query Match 47.4%; Score 37; DB 5; Length 639;
Best Local Similarity 46.7%; Pred. No. 1.2e+02; 0; Mismatches 8; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GSGXXXXGGPISSEQE 17
Db 623 GGGGSGASGGTIEE 637

RESULT 7
US-60-423-552-126

; Sequence 126, Application US/60423552

; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEP
; FILE REFERENCE: AMI01250L
; CURRENT APPLICATION NUMBER: US/60/423,552
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 256

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE: MISC_FEATURE
; NAME/KEY: MISC_FEATURE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2133

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On protein - protein search, using sw model

Run on: January 7, 2003, 12:28:08 ; Search time 13.1538 Seconds
 (without alignments)
 138.861 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 78 Sequence: 1 MDGSXXXXGGPISSEQI 19

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR_73;*

1: Pir1;*
 2: Pir2;*
 3: Pir3;*
 4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	69	88.5	192	bcl-2-associated protein x
2	67	85.9	143	bcl-2-associated protein x
3	67	85.9	179	bcl-2-associated protein x
4	67	85.9	192	bcl-2-associated protein x
5	67	85.9	218	bcl-2-associated protein x
6	46	59.0	654	bcl-2-associated protein x
7	40	51.3	487	bcl-2-associated protein x
8	40	51.3	492	bcl-2-associated protein x
9	39	51.3	528	bcl-2-associated protein x
10	39	50.0	105	bcl-2-associated protein x
11	39	50.0	248	bcl-2-associated protein x
12	38	48.7	334	bcl-2-associated protein x
13	38	48.7	487	bcl-2-associated protein x
14	38	48.7	1398	bcl-2-associated protein x
15	38	48.7	2186	bcl-2-associated protein x
16	37	48.1	1018	bcl-2-associated protein x
17	37	47.4	321	bcl-2-associated protein x
18	37	47.4	324	bcl-2-associated protein x
19	37	47.4	328	bcl-2-associated protein x
20	37	47.4	580	bcl-2-associated protein x
21	37	47.4	602	bcl-2-associated protein x
22	37	47.4	618	bcl-2-associated protein x
23	37	47.4	618	bcl-2-associated protein x
24	37	47.4	618	bcl-2-associated protein x
25	37	47.4	618	bcl-2-associated protein x
26	37	47.4	639	bcl-2-associated protein x
27	36	46.2	197	bcl-2-associated protein x
28	36	46.2	221	bcl-2-associated protein x
29	46.2		T47351	bcl-2-associated protein x

ALIGNMENTS

RESULT 1	Query	Match	Length	DB ID	Description
DB7538	1	MDGSXXXXGGPISSEQI	19	19	bcl-2-associated protein x - mouse
N: Alternative names: BAX; programmed cell death membrane protein x					
C: Species: Mus musculus (house mouse)					
C: Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000					
C: Accession: D47538					
R: Olvtvai, Z. N.; Milliman, C.L.; Korsmeyer, S.J.					
C: Cell 74, 609-619, 1993					
A: Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis					
A: Reference number: A47538; MUID:93364978; PMID:8358790					
A: Accession: D47538					
A: Status: preliminary					
A: Molecule type: mRNA					
A: Residues: 1-192 <OLD>					
A: Cross-references: GB:L22472					
C: Genetics:					
A: Gene: bax					
C: Superfamily: bcl transforming protein					
Query Match	88.5%	Score 69;	DB 2;	Length 192;	
Best Local Similarity	73.7%	Pred. No. 1e-05;	Mismatches 0;	Indels 5;	Gaps 0;
Matches	14;	Conservative			
Qy	1	MDGSXXXXGGPISSEQI	19		
Db	1	MDGSXXXXGGPISSEQI	19		

RESULT 2

Query	Match	Length	DB ID	Description
138921	1	MDGSXXXXGGPISSEQI	19	bcl-2-associated protein x, delta
C: Species: Homo sapiens (man)				
C: Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000				
C: Accession: 138921				
R: Aptek, S.S.; Mattei, M.G.; Olsen, B.R.				
G: Genomics 26, 592-594, 1995				
A: Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a				
A: Reference number: 138921; MUID:95331797; PMID:7607685				
A: Accession: 138921				
A: Status: preliminary; nucleic acid sequence not shown; translation not shown				
A: Molecule type: mRNA				
A: Residues: 1-143 <RES>				
A: Cross-references: EMBL:U19599; NID:9841237; PIDN:AAC50142.1; PID:9841238				
C: Genetics:				
A: Gene: GDB:BAX				
A: Cross-references: GDB:228082; OMIM:600040				
A: Map Position: 19q13.3-19q13.4				
C: Superfamily: bcl transforming protein				

Query Match Score 85.9%; Score 67; DB 2; Length 143;

Best local Similarity 73.7%; Pred. No 1.8e-05; 0; Mismatches 5; Indels 0; Gaps 0;

Matches 14; Conservative 0;

RESULT 3

JCT255
Bax-delta protein - human
C;Species: Homo sapiens (man)
C;Accession: JCT255
R;Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A;Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A;Reference number: JCT255
A;Accession: JCT255
A;Molecule type: mRNA
A;Residues: 1-179 <SCH>
A;Cross-references: GDB:AF247393
A;Experimental source: cancer promyelocytic cells
C;Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It fur
cactivation.
C;Superfamily: bcl transforming protein
C;Keywords: transmembrane protein

Query Match 85.9%; Score 67; DB 2; Length 179;
Best Local Similarity 73.7%; Pred. No. 2.3e-05; 0; Mismatches 5; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 MDGSGXXXXXGGPTSSQI 19
Db 1 MDGSGEOPRGGGPTSSQI 19

RESULT 4

A47538
bcl-2-associated protein x, alpha splice form - human
N;Alternate names: BAX, programmed cell death membrane protein x alpha
C;Species: Homo sapiens (man)
C;Accession: A47538
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 603-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
A;Reference number: A47538; MUID:9334978; PMID:8358790
A;Accession: A47538
A;Molecule type: mRNA
A;Residues: 1-192 <OLT>
A;Cross-references: GB:L22473; NID:9388165; PIDN:AAA03619.1; PMID:9388166
A;Note: the amino end of the mature protein is blocked
C;Genetics:
A;Gene: GDB:BAX
A;Cross-references: GDB:228082; OMIM:600040
A;Map position: 19q13.3-19q13.4
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; F;172-191/Domain: transmembrane #status predicted <TMH1>

Query Match 85.9%; Score 67; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 2.5e-05; 0; Mismatches 5; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 MDGSGXXXXXGGPTSSQI 19
Db 1 MDGSGEOPRGGGPTSSQI 19

RESULT 5

B47538
bcl-2-associated protein x, beta splice form - human

N;Alternate names: BAX; programmed cell death membrane protein x beta
C;Species: Homo sapiens (man)
C;Accession: B47538
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate
A;Reference number: A47538; MUID:93364978; PMID:8358790
A;Accession: B47538
A;Molecule type: mRNA
A;Residues: 1-218 <OLT>
A;Cross-references: GDB:L22474; NID:9388167; PIDN:AAA03620.1; PMID:9388168
C;Genetics:
A;Gene: GDB:BAX
A;Cross-references: GDB:228082; OMIM:600040
A;Map position: 19q13.3-19q13.4
A;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 85.9%; Score 67; DB 2; Length 218;
Best Local Similarity 73.7%; Pred. No. 2.9e-05; 0; Mismatches 5; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 MDGSGXXXXXGGPTSSQI 19
Db 1 MDGSGEOPRGGGPTSSQI 19

RESULT 6

S27004
shak-type molecular chaperone hsp70.1 - Hydra magnipapillata
N;Alternate names: heat shock protein 70.1
C;Species: Hydra magnipapillata
C;Accession: S27004
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C;Accession: S27004
R;Gellner, K.; Praetzel, G.; Bosch, T.C.G.
Eur. J. Biochem. 210, 683-691, 1992
A;Title: Cloning and expression of a heat-inducible hsp70 gene in two species of Hydr
A;Reference number: S27004; MUID:93130891; PMID:1483453
A;Accession: S27004
A;Molecule type: DNA
A;Residues: 1-654 <GET>
A;Cross-references: EMBL:M84019; NID:9159267; PIDN:AAA2913.1; PMID:9159268
C;Genetics:
A;Gene: hsp70.1
A;Introns: 69/1; 93/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 59.0%; Score 46; DB 2; Length 654;
Best Local Similarity 52.9%; Pred. No. 1.1; 0; Mismatches 9; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 MDGSGXXXXXGGPTSE 17
Db 636 MDGSGKASGGPTIE 652

RESULT 7

S21886
hypothetical protein HRX1851.1 - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Accession: S59162; S51886
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including t
a delta element.
A;Reference number: S59156; MUID:96076631; PMID:7502582

A;Accession: S59162
A;Status: nucleic acid sequence not shown; translation not shown; conceptual translation
A;Molecule type: DNA
A;Residues: 1-487 <VAV>
A;Cross-references: EMBL:248149; NID:9663234; PIDN:CAA88149.1; PID:9663241
C;Comment: There is no evidence that this sequence is expressed.
C;Genetics:
A;Map position: 15L
A;Introns: 472/2
C;Keywords: pseudogene

Query Match 51.3%; Score 40; DB 4; Length 487;
Best Local Similarity 38.9%; Pred. No. 11; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Oy 1 MDGSGXXXXGGPTSSBO 18
Db 310 MNNGNGSTDQISGPASGE 327

RESULT 8

S51885
probable membrane protein YOL112w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRC492; hypothetical protein 00726
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 20-Oct-2000
C;Accession: S51885; S59161; S66808
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, January 1995
A;description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including
and a Delta.
A;Reference number: S51848
A;Accession: S51885
A;Molecule type: DNA
A;Residues: 1-492 <VAN>
A;Cross-references: EMBL:248149; NID:9663234; PID:9663240
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995

A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the
a delta element.
A;Reference number: S59156; MUID:96076631; PMID:7502582
A;Accession: S59163
A;Status: nucleic acid sequence not shown; translation not shown; conceptual translation
A;Molecule type: DNA
A;Residues: 1-528 <VAV>
A;Cross-references: EMBL:248149; NID:9663234; PIDN:CAA88150.1; PID:9663242
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C;Comment: There is no evidence that this sequence is expressed.
C;Genetics:
A;Map position: 15L
A;Introns: 472/2
C;Keywords: pseudogene

RESULT 9

S51887
hypothetical protein HRX185I.2 - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000
C;Accession: S59163; S51887
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995

A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including t
a delta element.
A;Reference number: S59156; MUID:96076631; PMID:7502582
A;Accession: S59163
A;Status: nucleic acid sequence not shown; translation not shown; conceptual translat
A;Molecule type: DNA
A;Residues: 1-528 <VAV>
A;Cross-references: EMBL:248149; NID:9663234; PIDN:CAA88150.1; PID:9663242
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C;Comment: There is no evidence that this sequence is expressed.
C;Genetics:
A;Map position: 15L
A;Introns: 472/2
C;Keywords: pseudogene

RESULT 10

PW0018
hypothetical protein 105 - Micromonospora sp. (fragment)

C;Species: Micromonospora sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C;Accession: PW0018
R;Keleman, G.H.; Cundliffe, E.; Financek, I.
Gene 98, 53-60, 1991

A;Title: Cloning and characterization of gentamicin-resistance genes from Micromonosp
A;Reference number: JG0017; MUID:9192615; PMID:2013410
A;Accession: PW0018
A;Molecule type: DNA
A;Residues: 1-105 <KEL>

A;Cross-references: GB:M55521

A;Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a
Query Match 50.0%; Score 39; DB 2; Length 105;
Best Local Similarity 61.5%; Pred. No. 3.2; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 4 SGXXXXGGPSS 16

Db 74 SGCAATGGTSS 86

RESULT 11

F86743
hypothetical protein dacB [imported] - Lactococcus lactis subsp. lactis (strain IL140)

C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86743
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86743
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <STO>

A;Cross-references: GB:AE005176; PID:912723887; PIDN:AAK05048.1; GSPDB:GN00146
Oy 1 MDGSGXXXXGGPTSS 18

Db 310 MNNGNGSTDQISGPASGE 327

A;Experimental source: strain LL1403
 C;Genetics:
 A;Gene: dacB

Query Match 50.0%; Score 39; DB 2; Length 248;
 Best Local Similarity 38.9%; Pred. No. 8.2; Mismatches 9; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MDGSGXXXXGGPSSQ 18
 Db 134 MNGQCTVNNSGNPISSEE 151

RESULT 12
 A39605 transcriptions regulator *php2*, HAP2 homolog - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 31-Jan-2000
 C;Accession: A39605; T46663
 R;Olesen, J.T.; Files, J.D.; Guarente, L.
 Mol. Cell. Biol. 11, 611-619, 1991
 A;Title: The *Schizosaccharomyces pombe* homolog of *Saccharomyces cerevisiae* HAP2 reveals
 A;Reference number: A39605; MUID:9117227; PMID:1899284
 A;Accession: A39605
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-334 <OLE>
 A;Cross-references: GB:MG63639; NID:9173424; PIDN:AAA35322.1; PID:9173425
 R;Lynne, M.; Rajandream, M.A.; Barrell, B.G.; Rieder, M.
 submitted to the EMBL Data Library, November 1998
 A;Reference number: Z21889
 A;Accession: T46663
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-334 <LYN>
 A;Cross-references: EMBL:AL034352; PIDN:CAA22183 1; GSPPDB:GN00067; SPDB:SPBC725.11C
 A;Experimental source: strain 972h.; cosmid c725
 C;Genetics:
 A;Gene: SPBC725.11C
 A;Map position: 2
 C;Keywords: DNA binding; nucleus; transcription regulation

Query Match 48.7%; Score 38; DB 2; Length 487;
 Best Local Similarity 44.4%; Pred. No. 27; Mismatches 8; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MDGSGXXXXGGPSS 16
 Db 165 LDMSGNIAAMGGPNT 180

RESULT 13
 T47107 benzaldehyde dehydrogenase (NAD) (EC 1.2.1.28) [validated] - *Pseudomonas putida* plasmid
 C;Species: *Pseudomonas putida*
 C;Accession: T47107; S13388
 R;Inoue, J.; Shaw, J.P.; Rekk, M.; Hayayama, S.
 J. Bacteriol. 177, 1196-1201, 1995
 A;Title: Overlapping substrate specificity of benzaldehyde dehydrogenase (the *xylC* gene
Pseudomonas putida.
 A;Reference number: Z24352; MUID:95173094; PMID:7868591
 A;Accession: T47107
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-487 <INO>
 A;Cross-references: EMBL:U15151; NID:9555994; PIDN:AAA66218.1; PID:9555995
 R;Chalmers, R.M.; Keen, J.N.; Fewson, C.A.
 Biochem. J. 273, 99-107, 1991
 A;Title: Comparison of benzyl alcohol dehydrogenases and benzaldehyde dehydrogenases from
 A;Reference number: S13298; MUID:9113163; PMID:1989592
 A;Accession: S13388

Query Match 48.7%; Score 38; DB 2; Length 2186;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 T13741 hypothetical protein 22E5.8 - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C;Accession: T13741
 R;Murphy, L.; Harris, D.; Barrell, B.
 submitted to the EMBL Data Library, April 1999
 A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A;Reference number: Z17668
 A;Accession: T13741
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-1398 <MR>
 A;Cross-references: EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA21125.1
 C;Genetics:
 A;Cross-references: FlyBase:FBgn0006667
 A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
 A;Note: EG:22E5.8

Query Match 48.7%; Score 38; DB 2; Length 1398;
 Best Local Similarity 50.0%; Pred. No. 87; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DGSGXXXXGGPTS 15
 Db 851 NGGGSGNANGGPTS 864

RESULT 15
 T13169 tiggrin - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C;Accession: T13169
 R;Forserty, F.J.; Pessler, L.I.; Bunch, T.A.; Yaron, Y.; Parker, C.G.; Nelson, R.E.; Development, 120, 1747-1758, 1994
 A;Title: Tiggrin, a novel *Drosophila* extracellular matrix protein that functions as a
 A;Reference number: Z17625; MUID:90009506; PMID:7924982
 A;Accession: T13169
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 1-2186 <FOG>
 A;Cross-references: EMBL:U09506; NID:9493069; PID:9493070; PIDN:AAA56998.1
 C;Genetics:
 A;Cross-references: FlyBase:FBgn0011722
 C;Function:
 A;Description: functions as a ligand for *Drosophila* alpha PS2 beta PS integrins

Query Match 48.7%; Score 38; DB 2; Length 2186;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

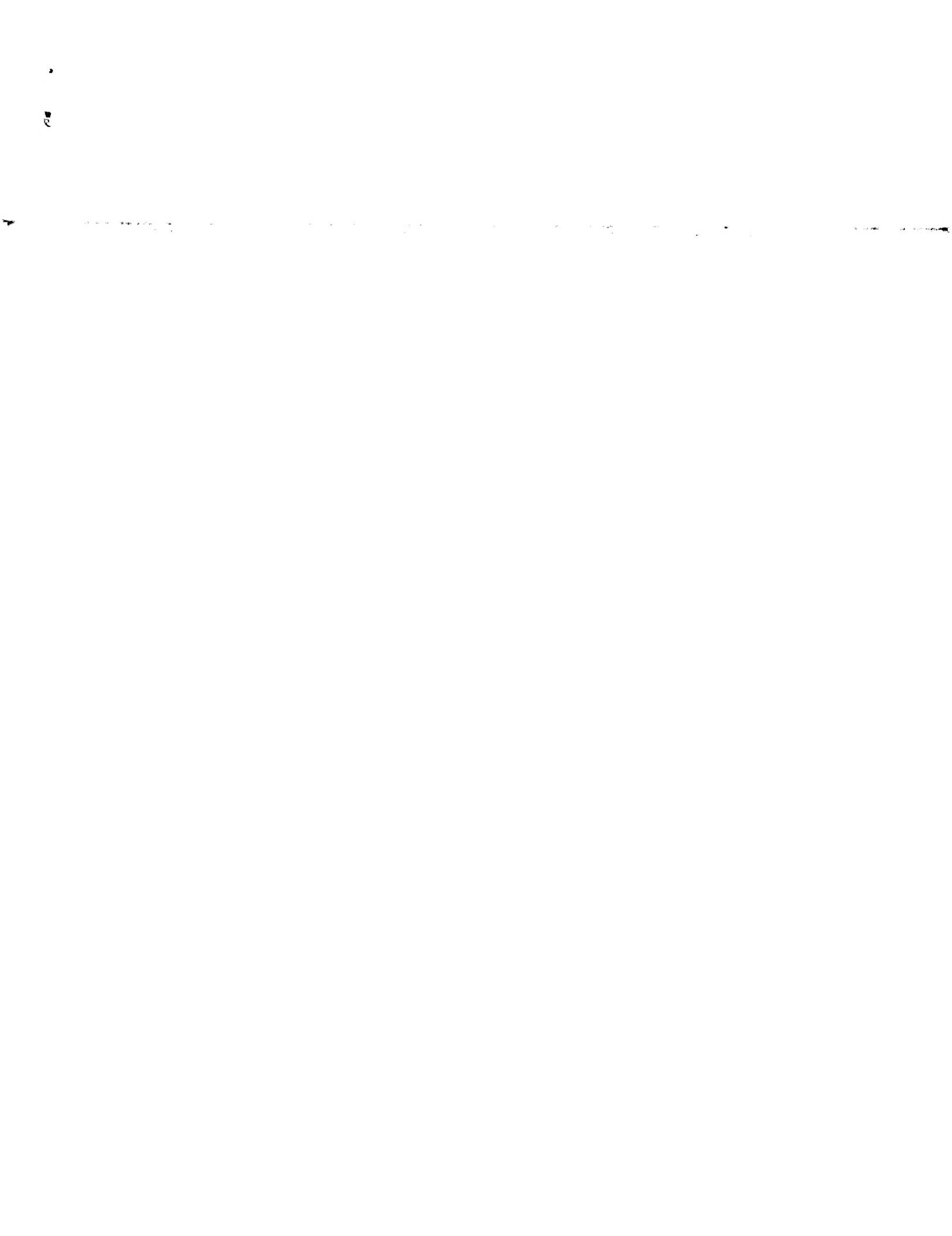
Tue Jan 7 13:10:47 2003

us-09-876-204-1_1.rpr

Page 5

Qy 3 GSGXXXXXGGPSS 16
||| |||
Db 2057 GSASASASGGPGS 2070

Search completed: January 7, 2003, 12:31:20
Job time : 15.1538 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:29:33 ; Search time 133 seconds
 (without alignments)
 92.105 Million cell updates/sec

Result No.	Score	Query Length	DB ID	Description
1	69	88.5	20	22 US-09-876-204-4
2	69	88.5	70	1 PCT-US99-24747-2
3	69	88.5	70	1 PCT-US99-24747-6
4	69	88.5	70	15 US-09-177-315-2
5	69	88.5	70	15 US-09-177-315-6
6	69	88.5	78	1 PCT-US99-24747-4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	69	88.5	20	22 US-09-876-204-4
2	69	88.5	70	1 PCT-US99-24747-2
3	69	88.5	70	1 PCT-US99-24747-6
4	69	88.5	70	15 US-09-177-315-2
5	69	88.5	70	15 US-09-177-315-6
6	69	88.5	78	1 PCT-US99-24747-4

RESULT¹ US-09-876-204-4

; Sequence 4, Application US/09876204

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09-876,204

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/165,028

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 4

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-876-204-4

Query Match Similarity Score 69; DB 22; Length 20;
 Best Local Similarity 73.7%; Pred. No. 7.5e-05; Mismatches 5; Indels 0; Gaps 0;

Matches	Conservative	Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli
Qy	1 MDGSGXXXXGGPITSSEQI 19					
Db	1 MDGSEQLGGGPITSSEQI 19					

Scoring table: BIOSIM62

Gapext 0.5

4569144 seqs, 64473110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pending Patents_AA_Main: *

1: /cgn2_6/pctodata/1/paa/PCTRUS_COMB.pep: *

2: /cgn2_6/pctodata/1/paa/us06_COMB.pep: *

3: /cgn2_6/pctodata/1/paa/us07_COMB.pep: *

4: /cgn2_6/pctodata/1/paa/us080_COMB.pep: *

5: /cgn2_6/pctodata/1/paa/us081_COMB.pep: *

6: /cgn2_6/pctodata/1/paa/us082_COMB.pep: *

7: /cgn2_6/pctodata/1/paa/us083_COMB.pep: *

8: /cgn2_6/pctodata/1/paa/us084_COMB.pep: *

9: /cgn2_6/pctodata/1/paa/us085_COMB.pep: *

10: /cgn2_6/pctodata/1/paa/us086_COMB.pep: *

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12: /cgn2_6/pctodata/1/paa/us088_COMB.pep: *

13: /cgn2_6/pctodata/1/paa/us089_COMB.pep: *

14: /cgn2_6/pctodata/1/paa/us090_COMB.pep: *

15: /cgn2_6/pctodata/1/paa/us092_COMB.pep: *

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24: /cgn2_6/pctodata/1/paa/us100_COMB.pep: *

25: /cgn2_6/pctodata/1/paa/us101_COMB.pep: *

26: /cgn2_6/pctodata/1/paa/us102_COMB.pep: *

27: /cgn2_6/pctodata/1/paa/us60_COMB.pep: *

ALIGNMENTS

RESULT 2
PCT-US99-24747-2
; Sequence 2, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/TUS99/24747
; CURRENT FILING DATE: 1999-10-22
; SEQ ID NO: 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-2

Query Match 88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MDGSGXXXGGPNSSEQI 19
Db 1 MDGSGEQLGSGGPNSSEQI 19

RESULT 3
PCT-US99-24747-6
; Sequence 6, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/TUS99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-6

Query Match 88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MDGSGXXXGGPNSSEQI 19
Db 1 MDGSGEQLGSGGPNSSEQI 19

RESULT 4
US-09-177-315-2
; Sequence 2, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-6

Query Match 88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MDGSGXXXGGPNSSEQI 19
Db 1 MDGSGEQLGSGGPNSSEQI 19

RESULT 5
US-09-177-315-6
; Sequence 6, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-6

Query Match 88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MDGSGXXXGGPNSSEQI 19
Db 1 MDGSGEQLGSGGPNSSEQI 19

RESULT 6
PCT-US99-24747-4
; Sequence 4, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/TUS99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-4

Query Match 88.5%; Score 69; DB 1; Length 78;
Best Local Similarity 73.7%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MDGSGXXXGGPNSSEQI 19
Db 1 MDGSGEQLGSGGPNSSEQI 19

RESULT 7
PCT-US99-24747-8
; Sequence 8, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/TUS99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34

Query Match 88.5%; Score 69; DB 15; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

US-08-112-208B-5
Sequence 5, Application US/08112208B
GENERAL INFORMATION:
APPLICANT: Korsmeyer, Stanley J.
TITLE OF INVENTION: Cell Death Regulators
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112, 208B
FILING DATE: 26-AUG-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-248-819-5
Query Match 88.5%; Score 69; DB 5; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096; Indels 0;
Matches 14; Conservative 0; Mismatches 5; Gaps 0;
OY 1 MDGSXXXXXGGTSSQI 19
Db 1 MDGSGEQLGGGPTSSQI 19
RESULT 13
US-08-248-819-5
Sequence 5, Application US/08248819
GENERAL INFORMATION:
APPLICANT: Korsmeyer, Stanley J.
TITLE OF INVENTION: Cell Death Regulators
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483, 233
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337, 646
FILING DATE: 10-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/248, 819
FILING DATE: 25-MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/112, 208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-000640
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "protein sequence of murine
1
2
3

; OTHER INFORMATION: Bax."

; US-08-483-233-3

	Query Match	Score 88.5%	DB 8	Length 192;
	Best Local Similarity	73.7%	Pred. No.	0.00096;
Matches	14;	Conservative	Mismatches	5;
			Indels	0;
QY	1 MDGSGXXXXXGGPTSEQI 19			0;
Db	1 MDGSGEQLGSGGPTSEQI 19			0;

RESULT 15

US-08-483-233-8

; Sequence 8; Application US/08483233

GENERAL INFORMATION:

APPLICANT: KORNMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0., version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,233

FILING DATE: HERMITH

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,646

FILING DATE: 10-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,819

FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/112,208

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000640

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-233-8

Query Match 88.5%; Score 69; DB 8; Length 192;

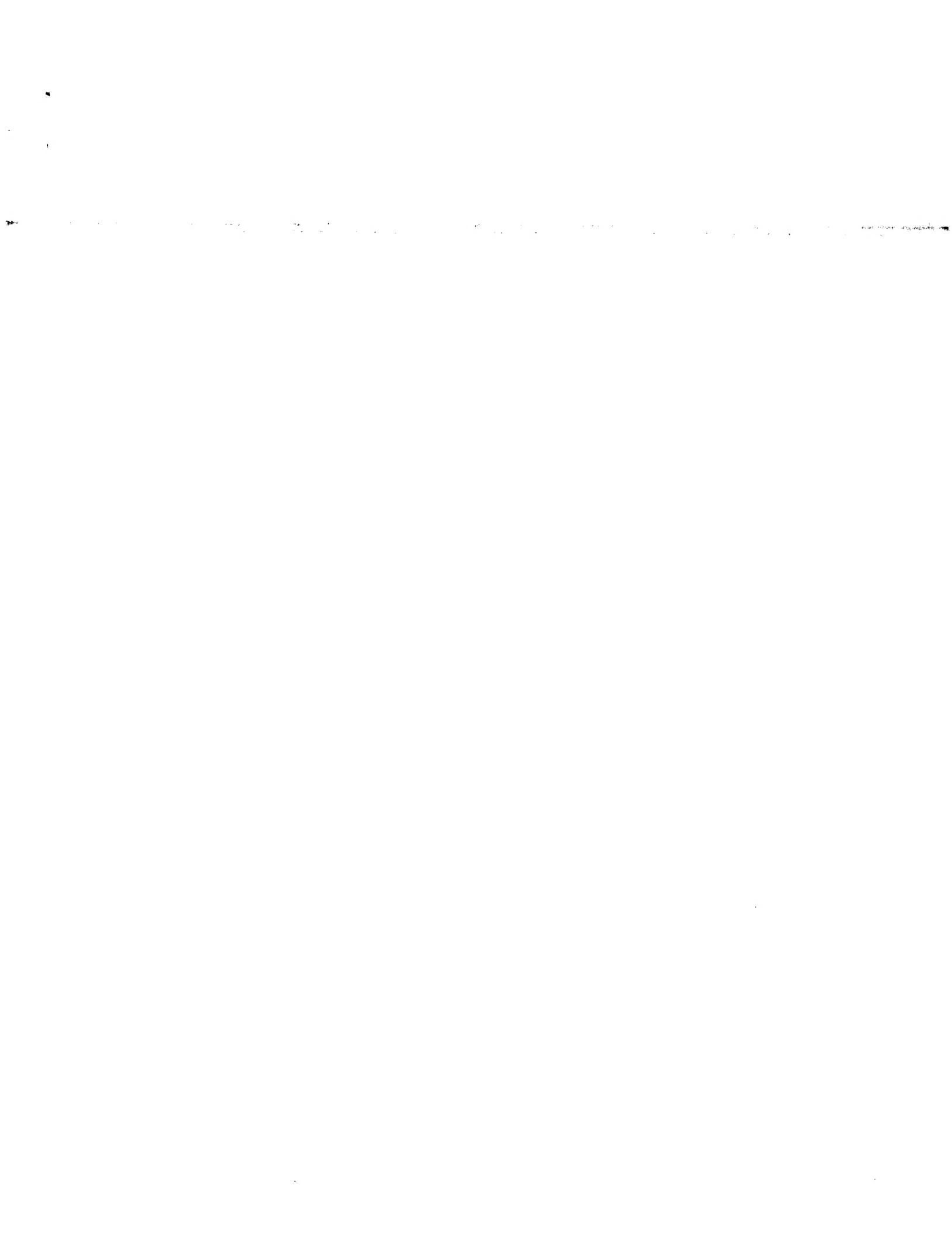
Best Local Similarity 73.7%; Pred. No. 0.00096;

Matches 14; Conservative 0; Mismatches 5; Indels 0;

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Db	1 MDGSGEQLGSGGPTSEQI 19

Search completed: January 7, 2003, 12:36:29

Job time : 134 secs



Run on: January 7, 2003, 12:30:53 ; Search time 7.30769 seconds
 (w/o alignments)
 49.274 Million cell updates/sec

OM protein - protein search, using sw model

Title:	January 7, 2003, 12:30:53 ; Search time 7.30769 seconds
Sequence:	US-09-876-204-1
Perfect score:	78
Sequence:	1 MSGGXXXXGGPTSSQI 19
Scoring table:	BIOSUM62
Gappop:	10.0 , Gapext 0.5
Searched:	117678 seqs, 18951520 residues
Total number of hits satisfying chosen parameters:	117078
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/prodata/1/pbpaa/us06_NEWPUB.pep:*
4: /cgn2_6/prodata/1/pbpaa/us05_NEWPUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	69	88.5	20	US-09-876-204-4
2	68	87.2	19	US-09-876-204-1
3	68	87.2	20	US-09-876-204-5
4	67	85.9	20	US-09-876-204-3
5	64	82.1	331	US-09-033-525-2
6	38	48.7	154	US-09-876-889-16
7	36	46.2	500	US-09-766-378A-25
8	36	46.2	547	US-09-815-837-90
9	36	46.2	553	US-09-815-837-50
10	36	46.2	555	US-09-815-837-71
11	36	46.2	559	US-09-815-837-96
12	36	46.2	560	US-09-815-837-72
13	36	46.2	562	US-09-815-837-70
14	36	46.2	676	US-09-815-837-69
15	36	46.2	678	US-09-815-837-68
16	36	46.2	772	US-09-815-837-74
17	36	46.2	774	US-09-815-837-72
18	35	44.9	46	US-09-889-919-115
19	44.9	473	10	US-09-844-353A-99

ALIGNMENTS

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RESULT 1
US-09-876-204-4
; Sequence 4, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09-876, 204
; CURRENT FILING DATE: 2001-06-06
; PRIORITY APPLICATION NUMBER: 09/166, 028
; PRIORITY FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-876-204-4
; Query Match 88.5%; Score 69; DB 10; Length 20;
; Best Local Similarity 73.7%; Pred. No. 9 2e-06;
; Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
; Qy 1 MDGSGXXXXGGPTSSQI 19
; Db 1 MDGSGEQLGSGGPTSSQI 19
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09-876, 204
; CURRENT FILING DATE: 2001-06-06
; PRIORITY APPLICATION NUMBER: 09/166, 028

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PRIOR FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic based on consensus sequence of Homo
 OTHER INFORMATION: sapiens, Mus musculus, and Rattus norvegicus
 NAME/KEY: VARIANT
 LOCATION: (6)..(10)
 OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
 OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
 OTHER INFORMATION: Xaa at 10 can be S or G;

Query Match, Best Local Similarity 100.0%; Score 68; DB 10; Length 19;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSXXXXGGGTSSQI 19
 DB 1 MDGSXXXXGGGTSSQI 19

RESULT 3
 US-09-876-204-5
 Sequence 5, Application US/09876204
 ; Patent No. US2002005316A1
 GENERAL INFORMATION:
 APPLICANT: Gordon C. Shore et al.
 TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
 FILE REFERENCE: 5013/011001
 CURRENT APPLICATION NUMBER: US/09/876,204
 CURRENT FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: 09/166,028
 PRIOR FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 20
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-876-204-5

Query Match, Best Local Similarity 87.2%; Score 68; DB 10; Length 20;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDGSXXXXGGGTSSQI 19
 DB 1 MDGSXXXXGGGTSSQI 19

RESULT 4
 US-09-876-204-3
 Sequence 3, Application US/09876204
 ; Patent No. US2002005316A1
 GENERAL INFORMATION:
 APPLICANT: Gordon C. Shore et al.
 TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
 FILE REFERENCE: 5013/011001
 CURRENT APPLICATION NUMBER: US/09/876,204
 CURRENT FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: 09/166,028
 PRIOR FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 20

Query Match, Best Local Similarity 87.2%; Score 68; DB 10; Length 19;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSXXXXGGGTSSQI 19
 DB 1 MDGSXXXXGGGTSSQI 19

RESULT 5
 US-09-033-525-2
 Sequence 2, Application US/09033525
 ; Patent No. US20020090374A1
 GENERAL INFORMATION:
 APPLICANT: Yarkoni, Shai
 APPLICANT: Ben Rehavah, Ahmi
 APPLICANT: Azar, Yerudit
 APPLICANT: Agelian, Rami
 APPLICANT: Beloitsotsky, Ruth
 APPLICANT: Lotberman-Galski, Haya
 TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING ACTIVITIES
 FILE REFERENCE: 9457-003-999
 CURRENT APPLICATION NUMBER: US/09/033,525
 CURRENT FILING DATE: 1998-03-02
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-033-525-2

Query Match, Best Local Similarity 85.9%; Score 67; DB 10; Length 20;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDGSXXXXGGPNSSEQI 19
 DB 1 MDGSGEQPRGGGTSSQI 19

RESULT 6
 US-09-876-889-16
 Sequence 16, Application US/09876889
 ; Patent No. US20020076715A1
 GENERAL INFORMATION:
 APPLICANT: Benson, Darin R.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Kling, Gordon E.
 APPLICANT: Compositions and Methods for Ovarian
 TITLE OF INVENTION: Cancer Therapy and Diagnosis
 FILE REFERENCE: 210121.466C3
 CURRENT APPLICATION NUMBER: US/09/876,889
 CURRENT FILING DATE: 2001-06-06
 NUMBER OF SEQ ID NOS: 353
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 16
 LENGTH: 154
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-876-889-16

Query Match, Best Local Similarity 48.7%; Score 38; DB 10; Length 154;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MDGSXXXXGGPNSSEQI 18

Db :||| 1 1 1: 72 LEGSGSAGEGKPAUSE 89

RESULT 7 Sequence 25, Application US/09766378A
 US-09-766-378A-25
 Patent No. US20020091079A1
 GENERAL INFORMATION:
 APPLICANT: Rhode, Peter R.
 Acevedo, Jorge
 Burkhardt, Martin
 Jiao, Jin an
 Wong, Hing C.

TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: usa

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSE for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,378A
 FILING DATE: 19-Jan-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/960,190
 FILING DATE: 29-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coriex, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 48002-DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 US-09-766-378A-25

Query Match 46.2%; Score 36; DB 10; Length 547;
 Best Local Similarity 53.3%; Pred No. 79;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy ||| 1 1 1: 3 GSGXXXXGGPSSSE 17
 Db 235 GSGGGGGGGSSSE 249

Query Match 46.2%; Score 36; DB 10; Length 547;
 Best Local Similarity 53.3%; Pred No. 79;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy ||| 1 1 1: 3 GSGXXXXGGPSSSE 17
 Db 235 GSGGGGGGGSSSE 249

RESULT 9 Sequence 50, Application US/09815837
 US-09-815-837-50

FILE REFERENCE: 014058-005670US
 CURRENT APPLICATION NUMBER: US/09/815,837

PATENT NO. US20020082411A1

GENERAL INFORMATION:

APPLICANT: Carter, Darrick
 APPLICANT: Zhu, Shirley
 APPLICANT: Arimilli, Subhashini
 APPLICANT: Wang, Ajun

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Immune Mediators and Related Methods

FILE REFERENCE: 014058-005670US
 CURRENT APPLICATION NUMBER: US/09/815,837

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 60/191,274

PRIOR FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: US 60/204,249

PRIOR FILING DATE: 2000-05-15

PRIOR APPLICATION NUMBER: US 60/264,003

PRIOR FILING DATE: 2001-01-23

NUMBER OF SEQ ID NOS: 129

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 50
 LENGTH: 553
 TYPE: PRM

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:I- As OTHER INFORMATION: MBP-beta1beta2alpha1alpha2_ck single chain OTHER INFORMATION: molecule

Query Match 46.2%; Score 36; DB 10; Length 553;
 Best Local Similarity 53.3%; Pred No. 80;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy ||| 1 1 1: 3 GSGXXXXGGPSSSE 17
 Db 241 GSGGGGGGGSSSE 255

RESULT 8 Sequence 90, Application US/09815837
 US-09-815-837-90

FILE REFERENCE: 014058-005670US
 CURRENT APPLICATION NUMBER: US/09/815,837

PATENT NO. US20020082411A1

GENERAL INFORMATION:

APPLICANT: Carter, Darrick
 APPLICANT: Zhu, Shirley
 APPLICANT: Arimilli, Subhashini

APPLICANT: Wang, Ajun

RESULTS 10

US-09-815-837-71 ; Sequence 71, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Ajun
; ORGANISM: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815, 837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191, 274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204, 249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264, 003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 71
; LENGTH: 555
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAs MBP 90-101
; OTHER INFORMATION: CH1_H recombinant MHC class II-peptide-Ig fusion
; OTHER INFORMATION: complex
; US-09-815-837-71
; RESULT 11
Query Match 46.2%; Score 36; DB 10; Length 555;
Best Local Similarity 53.3%; Pred. No. 80; Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GSXXXXXKGPTSE 17
Db 243 GSGGGGSGGGSSSE 257
; SEQ ID NO: 73
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAs MBP 1-14
; OTHER INFORMATION: CH1_H.CH2 recombinant MHC class II-peptide-Ig fusion complex
; OTHER INFORMATION: fusion complex
; US-09-815-837-73
; RESULT 12
Query Match 46.2%; Score 36; DB 10; Length 555;
Best Local Similarity 53.3%; Pred. No. 81; Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GSXXXXXKGPTSE 17
Db 247 GSGGGGGGGSSSE 261
; SEQ ID NO: 73
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAs MBP 90-101
; OTHER INFORMATION: CH1_H recombinant MHC class II-peptide-Ig fusion
; OTHER INFORMATION: complex
; US-09-815-837-73
; RESULT 13
Query Match 46.2%; Score 36; DB 10; Length 560;
Best Local Similarity 53.3%; Pred. No. 81; Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GSXXXXXKGPTSE 17
Db 243 GSGGGGSGGGSSSE 257
; SEQ ID NO: 73
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAs MBP 90-101
; OTHER INFORMATION: CH1_H recombinant MHC class II-peptide-Ig fusion
; OTHER INFORMATION: complex
; US-09-815-837-73
; RESULT 14
Query Match 46.2%; Score 36; DB 10; Length 559;
Best Local Similarity 53.3%; Pred. No. 81; Length 559;

Sequence 65', App
Sequence 9622, A
Sequence 9622, A
Sequence 18710, A
Sequence 18710, A
Sequence 1619, Ap
Sequence 6331, Ap
Sequence 22306, A
Sequence 52306, A
Sequence 6331, Ap
Sequence 25053, A
Sequence 22053, A
Sequence 22223, A
Sequence 22223, A
Sequence 3327, Ap
Sequence 5227, Ap
Sequence 16184, A
Sequence 17216, A
Sequence 16184, A

; ORGANISM: Homo sapiens
 US-10-306-876-5

Query Match 100.0%; Score 20; DB 6; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7.4e-12; Length 192;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-10-196-793A-46
 Sequence 46, Application US/10196793A
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENBLUM, MARTIN G.
 ; APPLICANT: LIU, YATING
 ; TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS
 ; CURRENT APPLICATION NUMBER: US/10/196,793A
 ; PRIOR APPLICATION NUMBER: 6/0/360,361
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/7332,886
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/305,091
 ; PRIOR FILING DATE: 2001-07-17
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 46
 ; LENGTH: 191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-196-793A-46

Query Match 95.0%; Score 19; DB 6; Length 191;
 Best Local Similarity 100.0%; Pred. No. 6.4e-11; Length 191;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DSGEOPRGGPPSSEQIM 20
 Db 1 DSGEOPRGGPPSSEQIM 19

RESULT 4
 US-09-134-000C-4348
 Sequence 4348, Application US/09134000C
 ; GENERAL INFORMATION:
 ; APPLICANT: LYNN DOUTETTE-STAMM et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-06-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6012
 ; SOFTWARE: PatentIn version 3.1.
 ; SEQ ID NO 4348
 ; LENGTH: 68
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 ; FEATURE:
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (44).(44)
 ; OTHER INFORMATION: Amino acid 44 is Xaa wherein Xaa = any amino acid.

Query Match 30.0%; Score 6; DB 5; Length 68;
 Best Local Similarity 100.0%; Pred. No. 54; Length 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 30.0%; Score 6; DB 5; Length 68;
 Best Local Similarity 100.0%; Pred. No. 54; Length 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-10-057-498-10714
 Sequence 10714, Application PC/TUS0232727
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: Blattia, Ajay
 ; APPLICANT: Maisonneuve, Jean Francois
 ; APPLICANT: Zhang, Yanni
 ; APPLICANT: Wang, Siqing
 ; APPLICANT: Jen, Shyian
 ; APPLICANT: Lodes, Michael
 ; APPLICANT: Benson, Darin
 ; APPLICANT: Jones, Robert
 ; APPLICANT: Carter, Barrick
 ; APPLICANT: Barth, Brenda
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514C1
 ; CURRENT APPLICATION NUMBER: PCT/US02/32727
 ; CURRENT FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 30992
 ; SEQ ID NO 10714
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 PCT-US02-32727-10714

Query Match 30.0%; Score 6; DB 1; Length 94;
 Best Local Similarity 100.0%; Pred. No. 67; Length 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTTSE 17
 Db 25 GGGPTS 30

RESULT 6
 US-10-057-498-10714
 Sequence 10714, Application US/10057498
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Persing, David
 ; APPLICANT: David
 ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
 ; FILE REFERENCE: 210121.514
 ; CURRENT APPLICATION NUMBER: US/10/057,498
 ; CURRENT FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 29212
 ; SEQ ID NO 10714
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: Propioni acnes
 US-10-057-498-10714

Query Match 30.0%; Score 6; DB 6; Length 94;
 Best Local Similarity 100.0%; Pred. No. 67; Length 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTTSE 17
 Db 30 GPTTSE 35

RESULT 7
 US-10-092-411A-5332
 Sequence 5332, Application US/10092411A

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: 032796-101
 CURRENT APPLICATION NUMBER: US/10/092,411A
 CURRENT FILING DATE: 2002-03-07
 PRIOR APPLICATION NUMBER: US 09/134,001
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5676
 SEQ ID NO: 5332
 LENGTH: 120
 TYPE: PRT
 ORGANISM: *Staphylococcus epidermidis*
 US-10-092,411A-5332

Query Match 30.0%; Score 6; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 13 PTSSeq 18
 Db 54 PTSSeq 59

RESULT 8
 US-60-425-158-26
 ; Sequence 26, Application US/60425158
 ; GENERAL INFORMATION:
 ; APPLICANT: Rupp, Fabio
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 ; FILE REFERENCE: HYS-66
 ; CURRENT APPLICATION NUMBER: US/60/425,158
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/5560,875
 ; PRIOR FILING DATE: 2000-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/323,349
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/03800
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 50
 ; SEQ ID NO: 26
 ; LENGTH: 134
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-425-158-26

Query Match 30.0%; Score 6; DB 7; Length 155;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 GSSEQP 8
 Db 79 GSSEQP 84

RESULT 10
 US-60-425-158-31
 ; Sequence 31, Application US/60425158
 ; GENERAL INFORMATION:
 ; APPLICANT: Rupp, Fabio
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 ; FILE REFERENCE: HYS-66
 ; CURRENT APPLICATION NUMBER: US/60/425,158
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: 10/245,817
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; SEQ ID NO: 23
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-425-158-31

Query Match 30.0%; Score 6; DB 7; Length 134;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 GSSEQP 8
 Db 79 GSSEQP 84

RESULT 9
 US-60-425-158-23
 ; Sequence 23, Application US/60425158
 ; GENERAL INFORMATION:
 ; APPLICANT: Rupp, Fabio
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 ; FILE REFERENCE: HYS-66
 ; CURRENT APPLICATION NUMBER: US/60/425,158
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/03800
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 09/5560,875
 ; PRIOR FILING DATE: 2000-01-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; SEQ ID NO: 23
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-425-158-23

Query Match 30.0%; Score 6; DB 7; Length 134;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 GSSEQP 8
 Db 79 GSSEQP 84

RESULT 10
 US-60-425-158-31
 ; Sequence 31, Application US/60425158
 ; GENERAL INFORMATION:
 ; APPLICANT: Rupp, Fabio
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 ; FILE REFERENCE: HYS-66
 ; CURRENT APPLICATION NUMBER: US/60/425,158
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: 10/245,817
 ; PRIOR FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/245,819
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; SEQ ID NO: 23
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-425-158-31

Query Match 30.0%; Score 6; DB 7; Length 134;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: PCT/US01/03623
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 09/491,404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: PCT/US01/03800
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 09/560,875
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 09/496,914
 PRIOR FILING DATE: 2000-02-03
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.1
 SBQ ID NO: 31
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-60-425-158-31

RESULT 11
 Query Match 30.0%; Score 6; DB 7; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	GSGEQP	8
Db	58	GSGEQP	63

US-60-425-158-38
 Sequence 38 Application US/60425158
 GENERAL INFORMATION:
 APPLICANT: Rupp, Fabio
 APPLICANT: Wang, Zhiwei
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 CURRENT APPLICATION NUMBER: PCT/US00/35017
 CURRENT FILING DATE: 2002-11-08
 PRIOR APPLICATION NUMBER: 10/245,817
 PRIOR FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/323,349
 PRIOR FILING DATE: 2001-09-18
 PRIOR APPLICATION NUMBER: US/60/425,158
 CURRENT FILING DATE: 2002-11-08
 PRIOR APPLICATION NUMBER: 10/245,817
 PRIOR FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 60/323,349
 PRIOR FILING DATE: 2001-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/35017
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: PCT/US01/03623
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 09/491,404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: PCT/US01/03800
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 09/560,875
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 09/496,914
 PRIOR FILING DATE: 2000-02-03
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.1
 SBQ ID NO: 28
 LENGTH: 176
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-60-425-158-28

RESULT 13
 Query Match 30.0%; Score 6; DB 7; Length 176;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	GSGEQP	8
Db	79	GSGEQP	84

US-60-425-158-35
 Sequence 35 Application US/60425158
 GENERAL INFORMATION:
 APPLICANT: Rupp, Fabio
 APPLICANT: Wang, Zhiwei
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
 CURRENT APPLICATION NUMBER: US/60/425,158
 CURRENT FILING DATE: 2002-11-08
 PRIOR APPLICATION NUMBER: 10/245,817

Remaining Prior Application data removed - See File Wrapper or PALM.

PRIOR APPLICATION NUMBER: 09/496,914
 PRIOR FILING DATE: 2000-02-03
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.1
 SBQ ID NO: 38
 LENGTH: 174
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-60-425-158-38

PRIOR FILING DATE: 2002-09-16 ; LENGTH: 195
PRIOR APPLICATION NUMBER: 60/323,349 ; TYPE: PRT
PRIOR FILING DATE: 2001-09-18 ; ORGANISM: Homo sapiens
PRIOR APPLICATION NUMBER: PCT/US00/35017 ; US-60-425-158-49
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/495,914
PRIOR FILING DATE: 2000-02-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 50
SOFTWARE: patentin version 3.1
SEQ ID NO: 35
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
; US-60-425-158-35

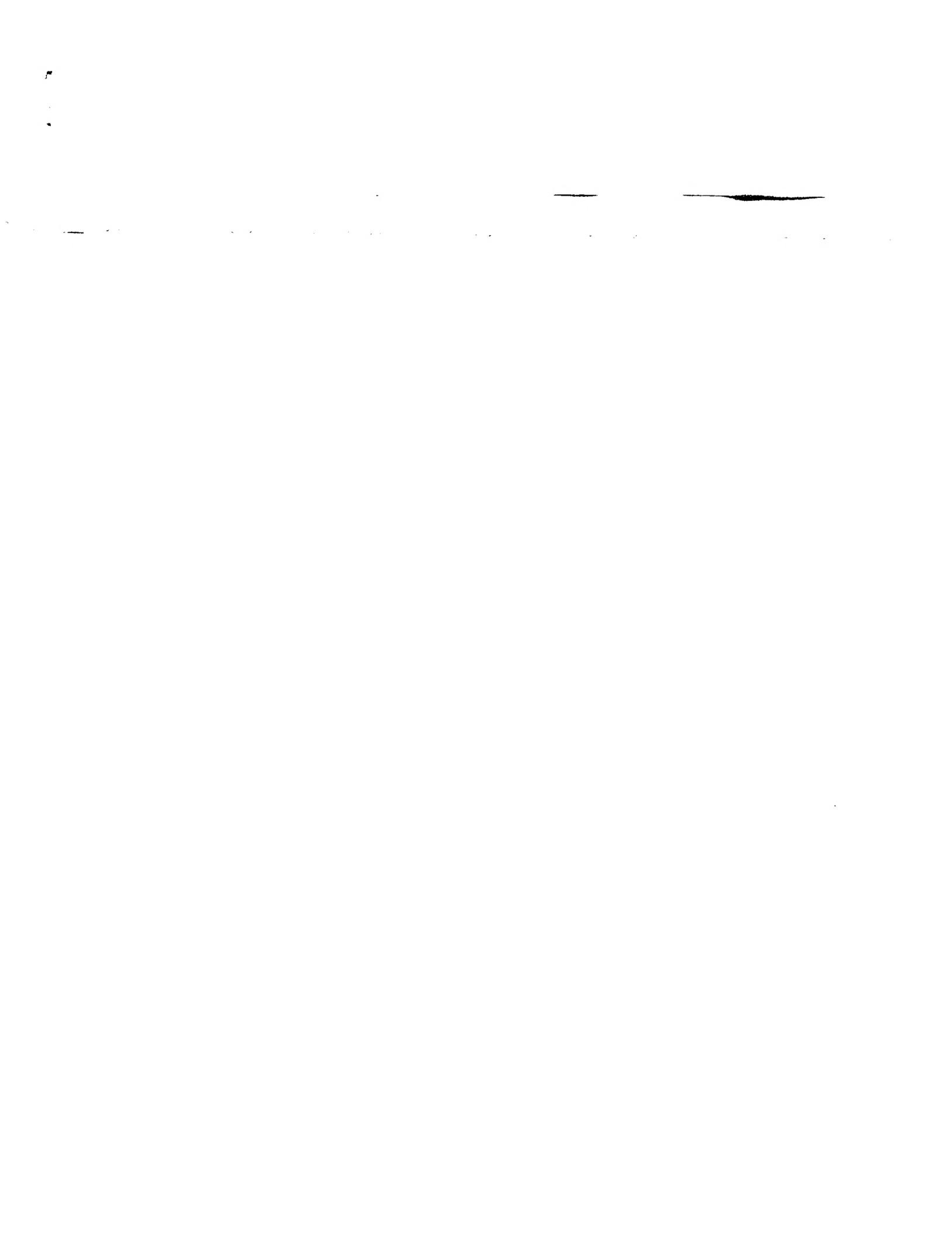
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 GSGEQP 8
Db 79 GSGEQP 84

RESULT 15 ; LENGTH: 195
US-09-724-676-55403 ; Sequence 55403, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 9722
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 55403
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676-55403

Query Match 30.0%; Score 6; DB 5; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 PRGGGP 13
Db 81 PRGGGP 86

Search completed: January 7, 2003, 12:46:01
Job time : 11.7949 secs

RESULT 14 ; LENGTH: 195
US-60-425-158-49
; Sequence 49, Application US/60425158
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; APPLICANT: Wang, Zhiwei
; APPLICANT: Rupp, Fabio
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; FILE REFERENCE: HYS-66
; CURRENT APPLICATION NUMBER: US/60/425,158
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 50
SOFTWARE: patentin version 3.1
SEQ ID NO: 49



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GenCore version 5.1.3

OM protein - protein search, using SW mode

Run on: January 7, 2003, 12:38:34 : Search time 140 Seconds
 (without alignments)

US-09-876-204-3
 (92.105 Million cell updates/sec)

Title: Perfect score:
 Sequence: US-09-876-204-3

Scoring table: OurGO
 Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/paa/US082_COMBO.pep:*

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8: /cgn2_6/ptodata/1/paa/US084_COMBO.pep:*

9: /cgn2_6/ptodata/1/paa/US085_COMBO.pep:*

10: /cgn2_6/ptodata/1/paa/US086_COMBO.pep:*

11: /cgn2_6/ptodata/1/paa/US087_COMBO.pep:*

12: /cgn2_6/ptodata/1/paa/US088_COMBO.pep:*

13: /cgn2_6/ptodata/1/paa/US089_COMBO.pep:*

14: /cgn2_6/ptodata/1/paa/US090_COMBO.pep:*

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17: /cgn2_6/ptodata/1/paa/US093_COMBO.pep:*

18: /cgn2_6/ptodata/1/paa/US094_COMBO.pep:*

19: /cgn2_6/ptodata/1/paa/US095_COMBO.pep:*

20: /cgn2_6/ptodata/1/paa/US097_COMBO.pep:*

21: /cgn2_6/ptodata/1/paa/US098_COMBO.pep:*

22: /cgn2_6/ptodata/1/paa/US099_COMBO.pep:*

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24: /cgn2_6/ptodata/1/paa/US101_COMBO.pep:*

25: /cgn2_6/ptodata/1/paa/US102_COMBO.pep:*

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27: /cgn2_6/ptodata/1/paa/US60_COMBO.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	20	100.0	20	22 US-09-876-204-3
2	20	100.0	70	1 PCT-US99-24747-3
3	20	100.0	70	1 PCT-US99-24747-5
4	20	100.0	70	1 US-09-177-315-1
5	20	100.0	70	1 US-09-177-315-5
6	20	100.0	78	1 PCT-US99-24747-3

ALIGNMENTS

RESULT 1
 US-09-876-204-3

; SEQUENCE 3, Application US/09876204

; GENERAL INFORMATION:

; APPLICANT: Gordon C. Shore et al.

; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATOR

; FILE REFERENCE: 50013/011001

; CURRENT APPLICATION NUMBER: US/09-876, 204

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/166, 028

; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-876-204-3

Query Match 100.0%; Score 20; DB 22;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;
 Matches 20; Conservative 0; Mismatches 0;

Qy 1 MDGSGEQPRGGGPTTSSEQIM 20
 Db 1 MDGSGEQPRGGGPTTSSEQIM 20

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ase : processing: Listing first 45 summaries

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3: /cgn2_6/podata/a/1/paa/US07_COMBO_PEP:*
4: /cgn2_6/podata/a/1/paa/US08_COMBO_PEP:*
5: /cgn2_6/podata/a/1/paa/US09_COMBO_PEP:*
6: /cgn2_6/podata/a/1/paa/US082_COMBO_PEP:*
7: /cgn2_6/podata/a/1/paa/US083_COMBO_PEP:*
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10: /cgn2_6/podata/a/1/paa/US086_COMBO_PEP:*
11: /cgn2_6/podata/a/1/paa/US087_COMBO_PEP:*
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23: /cgn2_6/podata/a/1/paa/US099_COMBO_PEP:*
24: /cgn2_6/podata/a/1/paa/US100_COMBO_PEP:*
25: /cgn2_6/podata/a/1/paa/US101_COMBO_PEP:*
26: /cgn2_6/podata/a/1/paa/US102_COMBO_PEP:*
27: /cgn2_6/podata/a/1/paa/US60_COMBO_PEP:*

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-876-204-3
; Sequence 3, Application US/09876204
; GENERAL INFORMATION:
; APPLICANT: GOTOGO C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876, 204
; CURRENT FILING DATE: 2001-05-06
; PRIORITY APPLICATION NUMBER: 09/166, 028
; PRIORITY FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-204-3

RESULT 2
PCT-US99-24747-1
; Sequence 1, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754.
CURRENT APPLICATION NUMBER: PCT/US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 1
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-1

Query Match 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGGSQOPRGGPTSSEQIM 20
Db 1 MDGGSQOPRGGPTSSEQIM 20

RESULT 3
PCT-US99-24747-5
; Sequence 5, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT/US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 5
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-5

Query Match 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGGSQOPRGGPTSSEQIM 20
Db 1 MDGGSQOPRGGPTSSEQIM 20

RESULT 4
US-09-177-315-1
; Sequence 1, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT/US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 3
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGGSQOPRGGPTSSEQIM 20
Db 1 MDGGSQOPRGGPTSSEQIM 20

RESULT 5
US-09-177-315-5
; Sequence 5, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1756
CURRENT APPLICATION NUMBER: US/09/177, 315
CURRENT FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 5
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
US-09-177-315-5

Query Match 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGGSQOPRGGPTSSEQIM 20
Db 1 MDGGSQOPRGGPTSSEQIM 20

RESULT 6
PCT-US99-24747-3
; Sequence 3, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT/US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 3
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match 100.0%; Score 20; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGGSQOPRGGPTSSEQIM 20
Db 1 MDGGSQOPRGGPTSSEQIM 20

RESULT 7
PCT-US99-24747-7
; Sequence 7, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT/US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34

RESULT 8
US-09-177-315-3
; Sequence 3, Application US/09177315
; GENERAL INFORMATION:
; Best Local Similarity 100.0%; Score 20; DB 1; Length 78;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US99-24747-7

Query Match 100.0%; Score 20; DB 1; Length 78;
Match 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; CURRENT APPLICATION NUMBER: US/09/177, 315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-177-315-3

RESULT 9
US-09-177-315-7
; Sequence 7, Application US/09177315
; GENERAL INFORMATION:
; Best Local Similarity 100.0%; Score 20; DB 15; Length 78;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; CURRENT APPLICATION NUMBER: US/09/177, 315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-177-315-7

Query Match 100.0%; Score 20; DB 15; Length 78;
Match 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; CURRENT APPLICATION NUMBER: US/09/177, 315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-177-315-7

RESULT 10
US-09-053-59-2
; Sequence 2, Application PC/TUS9905359
; GENERAL INFORMATION:
; Best Local Similarity 100.0%; Score 20; DB 15; Length 78;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; GENERAL INFORMATION:
; FILE REFERENCE: INGN:08B/INGN:08B
; CURRENT APPLICATION NUMBER: US/09/266, 465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077, 541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
; PCT-US99-05359-2

Query Match 100.0%; Score 20; DB 16; Length 131;
Match 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; GENERAL INFORMATION:
; FILE REFERENCE: INGN:08B/INGN:08B
; CURRENT APPLICATION NUMBER: US/09/266, 465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077, 541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
; PCT-US99-05359-2

RESULT 11
US-09-266-465-2
; Sequence 2, Application US/09266465
; GENERAL INFORMATION:
; Best Local Similarity 100.0%; Score 20; DB 1; Length 131;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; GENERAL INFORMATION:
; FILE REFERENCE: INGN:08B/INGN:08B
; CURRENT APPLICATION NUMBER: US/09/266, 465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077, 541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
; PCT-US99-05359-2

Query Match 100.0%; Score 20; DB 1; Length 131;
Match 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; GENERAL INFORMATION:
; FILE REFERENCE: INGN:08B/INGN:08B
; CURRENT APPLICATION NUMBER: US/09/266, 465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077, 541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
; PCT-US99-05359-2

FILE REFERENCE: 50036/050W02
 CURRENT APPLICATION NUMBER: PCT/US02/06951
 PRIOR APPLICATION NUMBER: US 60/274, 526
 PRIOR FILING DATE: 2001-03-08
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 242
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens

PCT-US02/06951-242

RESULT 13
 US-10-092-750-242
 Sequence 242, Application US/10092750
 GENERAL INFORMATION:
 APPLICANT: Hammond, Philip W.
 APPLICANT: Alpin, Julia
 APPLICANT: Wright, Martin C.
 TITLE OF INVENTION: Polypeptides Interactive with BCL-XL

FILE REFERENCE: 50036/050002
 CURRENT APPLICATION NUMBER: US 10/092, 750
 CURRENT FILING DATE: 2002-03-07
 PRIOR APPLICATION NUMBER: US 60/274, 526
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 253
 SEQ ID NO 242
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-092-750-242
 Software: FastSEQ for Windows Version 4.0
 SEQ ID NO 242
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 14
 US-09-791-537-52874
 Sequence 52874, Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Daner, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791, 537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2874
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-791-537-52874
 Query Match 100.0%; Score 20; DB 21; Length 143;

Query Match 100.0%; Score 20; DB 27; Length 143;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGPNSSEQIM 20
 Db 1 MDGSGEQPRGGPNSSEQIM 20

RESULT 15
 US-60-350-061-261
 Sequence 261, Application US/60350061
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH SRC TYROSINE KINASES AND THE SRC TYROSINE KINASE
 FILE REFERENCE: D0185
 CURRENT APPLICATION NUMBER: US 60/355, 061
 CURRENT FILING DATE: 2002-01-18
 NUMBER OF SEQ ID NOS: 981
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 261
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Homo sapiens

US-60-350-061-261
 Query Match 100.0%; Score 20; DB 27; Length 143;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGPNSSEQIM 20
 Db 1 MDGSGEQPRGGPNSSEQIM 20

Search completed: January 7, 2003, 12:45:31
 Job time : 140 secs

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Run on:	January 7, 2003, 12:25:07 : Search time 7.30769 Seconds (without alignments) 107.838 Million cell updates/sec		
On protein - protein search, using sw model			
Title:	US-09-876-204-1		
Perfect score:	78		
Sequence:	1 MDCGGXXXXGGPSSFOI 19		
Scoring table:	BLOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	112892 seqs, 41476328 residues		
Total number of hits satisfying chosen parameters:	112892		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Minimum Match 0 %		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	SwissProt_40: *		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
	SUMMARIES		
Result No.	Score	Query Match Length DB ID	Description
1	69	88.5 192 1 BAXA_MOUSE	Q07813 mus musculus
2	68	87.2 192 1 BAXA_RAT	Q63690 rattus norvegicus
3	67	85.9 143 1 BAXD_HUMAN	P55269 homo sapien
4	67	85.9 192 1 BAXA_BOVINE	Q02703 bos taurus
5	67	85.9 192 1 BAXB_HUMAN	Q07812 homo sapien
6	67	85.9 218 1 BAXB_BOVINE	Q07814 homo sapien
7	59.0 654 1 H570_HDMMA	Q05944 hydra magnifica	
8	59.0 105 1 YGRM_MICROB	P24621 microcionosp	
9	38.7 334 1 PHR2_SCOPHO	P24488 schizosaccharomyces pombe	
10	38.7 487 1 XTC_PSEPPU	P43503 pseudomonas aeruginosa	
11	37.4 321 1 ISP_BACCS	P29140 bacillus cereus	
12	37.4 579 1 YH83_SCOPHO	Q9Pn2 schizosaccharomyces pombe	
13	37.4 602 1 GAP1_YEAST	P19145 saccharomyces cerevisiae	
14	37.4 618 1 SPAA_ECOLI	P08395 escherichia coli	
15	37.4 631 1 HST3_BOVINE	P34933 bos taurus	
16	37.4 639 1 HST2_HUMAN	P54652 homo sapien	
17	36.2 109 1 PER_RHACO	Q26231 rhabdolites perrieri	
18	36.2 450 1 SPP1_ENCUU	Q9xzv1 encephalitozoon cuniculi	
19	36.2 574 1 ME22_SCOPHO	Q06170 schizosaccharomyces pombe	
20	36.2 862 1 POIG_ECOLI	Q66790 echovirus 1	
21	36.2 1185 1 DRPL_HUMAN	P54259 homo sapien	
22	35.9 44.9 473 1 HN32A_HUMAN	P55317 homo sapien	
23	35.9 44.9 474 1 MERA_STRL1	P30341 streptomyces	
24	35.9 44.9 512 1 GME2_MOUSE	P58929 mus musculus	
25	35.9 44.9 529 1 GHM2_RAT	Q88873 rattus norvegicus	
26	35.9 44.9 530 1 GM22_HUMAN	Q9ukdl1 homo sapien	
27	35.9 44.9 633 1 HS72_MOUSE	P17156 mus musculus	
28	35.9 44.9 633 1 HS72_RAT	P14659 rattus norvegicus	
29	35.9 44.9 880 1 TY03_MOUSE	P55144 mus musculus	
30	35.9 44.9 1709 1 CHD1_HUMAN	Q164645 homo sapien	
31	34.6 154 1 NEU1_CATCO	P15210 catostomus	
32	34.6 176 1 VLP_A_MCHR	P29228 mycoplasma pneumoniae	
33	34.6 1 COAT_OVMW	P20124 ononis yellows	
		ALIGNMENTS	
34	34	43.6 347 1 UTR2_YEAST	P32623 saccharomyces cerevisiae
35	34	43.6 351 1 E2BB_HUMAN	P49770 homo sapiens
36	34	43.6 359 1 Y199_MICCTU	P07733 mycobacterium
37	34	43.6 370 1 CICB_PSEPU	P11452 pseudomonas
38	34	43.6 382 1 ND12_HUMAN	Q15784 homo sapiens
39	34	43.6 382 1 NDE2_RAT	Q63689 rattus norvegicus
40	34	43.6 383 1 ND12_MOUSE	Q62414 mus musculus
41	34	43.6 384 1 HEM2_DRONE	Q9v9s8 drosophila melanogaster
42	34	43.6 401 1 ENO_THEVO	Q979z9 thermoplasma acidophilum
43	34	43.6 426 1 YF26_MYCTU	P05081 mycobacterium
44	34	43.6 468 1 HNFA_MOUSE	P35582 mus musculus
45	34	43.6 506 1 NP13_HUMAN	Q99457 homo sapiens

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 CC ALTERNATIVE SPlicing.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC
 EMBL: U19599; AAC50142.1; - .
 DR Genew; HGNC: 959; BAX.
 DR MIM: 600040; - .
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR InterPro; IPR000712; Bcl2_BH.
 DR Pfam; PF00452; Bcl-2; 1.
 DR PROSITE; PS00337; BCL; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 KW Apoptosis; Alternative splicing.
 FT DOMAIN 49 69 BH1.
 SEQUENCE 143 AA: 15772 MW: BADE4D71D06A75AB CRC64;
 Query Match 85.9%; Score 67; DB 1; Length 143;
 Best Local Similarity 73.7%; Pred. No. 9.9e-06; 5; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 Qy 1 MDGSGXXXXXGGPTSSQI 19
 Db 1 MDGSGGPORGGGTSSQI 19
 RESULT 4
 BAXA_BOVIN STANDARD; PRT; 192 AA.
 ID BAXA_BOVIN AC 002703;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE Apoptosis regulator BAX, membrane isoform alpha.
 GN BAX.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID:9913;
 RN [1] SEQUENCE FROM N A.
 RC STRAIN=Holstein; TISSUE=thymus;
 RX MEDLINE=98162580; PubMed=9501056;
 RA Reyes R. A.; Cockrell G.L.;
 RT "Increased ratio of bcl-2/bax expression is associated with bovine
 RT leukemia virus induced leukemogenesis in cattle.";
 RT Virology 242:184-192(1998).
 CC
 CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C'
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
 CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
 CC CESATION OF SPERM PRODUCTION (BY SIMILARITY).
 CC
 CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERO DIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
 CC -!- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC
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 CC
 EMBL: U92569; AAC48806.1; - .
 DR HSPP; Q07817; IM2.
 DR InterPro; IPR002475; BCL2_FAMILY.
 DR InterPro; IPR000712; Bcl2_BH.
 DR Pfam; PF00452; Bcl-2; 1.
 DR SMART; SM00337; BCL; 1.
 DR PROSITE; PS00337; BCL; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS0062; BCL2_FAMILY; 1.
 FT DOMAIN 59 73 BH2.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT DOMAIN 172 192 BH1.
 SEQUENCE 192 AA: 21259 MW: 6B4D5BABF1D5F87E CRC64;
 Query Match 85.9%; Score 67; DB 1; Length 192;
 Best local Similarity 73.7%; Pred. No. 1.4e-05; 5; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 Qy 1 MDGSGXXXXXGGPTSSQI 19
 Db 1 MDGSGGPORGGGTSSQI 19
 RESULT 5
 BAXA_HUMAN STANDARD; PRT; 192 AA.
 ID BAXA_HUMAN AC 007812;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator BAX, membrane isoform alpha.
 GN BAX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1] SEQUENCE FROM N A.
 RP SSEQUENCE FROM N A.
 RC TISSUE-B-cell;
 RX MEDLINE=93364978; PubMed=9358790;
 RA Ottvai Z.N.; Milliman C.L.; Korsmeyer S.J.;
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 accelerates programmed cell death.";
 RL Cell 74:609-619(1993).
 RN [2] MOTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
 RP MEDLINE=96091131; PubMed=9521816;
 RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
 RA Elangovan B., Chinnadurai G., Lutz R.J.;
 RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell
 RT death and protein binding functions.";
 RL FEMO J. 14:5589-5596(1995).
 RN [3] VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC

		Db	RESULT 6
SQ	SEQUENCE	ID	BAXB_HUMAN
CC	Blood 91; 2991-2997 (1998).	AC	STANDARD;
CC	-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG B1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THERAPY APOPTOSIS.	AC	PRT; 218 AA.
CC	-!- SUBUNIT: FORMS HOMODIMERS AND HETERO DIMERS TOGETHER WITH BCL-2, B1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL.	AC	
CC	-!- SUBCELLULAR LOCATION: Membrane-bound.	AC	
CC	-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.	AC	
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.	AC	
CC	-!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.	AC	
CC	-!- DISEASE: Defects in BAX are found in some cell lines from hematopoietic malignancies as T-cell acute lymphoblastic leukemia, Burkitt lymphoma, and plasmacytoma.	AC	
CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH2) DOMAIN.	AC	
CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.	AC	
CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.	AC	
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.	AC	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).	AC	
CC	CC	RL	SEQUENCE FROM N.A.
CC	CC	RC	TISSUE=B-cell;
CC	CC	RX	MEDLINE93364978; PubMed=8358790;
CC	CC	RA	Oltval A.N., Millman C.L., Korsmeyer S.J.;
CC	CC	DT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC	CC	DE	APOPTOSIS regulator BAX, cytoplasmic isoform beta.
CC	CC	RN	[1]
CC	CC	GN	BAX.
CC	CC	OS	Homo sapiens (Human).
CC	CC	OC	Cell 74:659-619(1993).
CC	CC	OC	-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG B1B 19K PROTEIN.
CC	CC	CC	-!- SUBUNIT: FORMS HOMODIMERS AND HETERO DIMERS TOGETHER WITH BCL-2, B1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL.
CC	CC	CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.
CC	CC	CC	-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
CC	CC	CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC	CC	CC	-!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC	CC	CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 1 (BH1) DOMAIN.
CC	CC	CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 2 (BH2) DOMAIN.
CC	CC	CC	-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY 3 (BH3) DOMAIN.
CC	CC	CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).
CC	CC	CC	EMBL: L22474; AAA03619.1; -.
DR	DR	DR	PIR: A47538; Bcl2_BH.
DR	DR	DR	HSSP; Q07817; IMAZ.
DR	DR	DR	SMART; SM00337; BCL; 1.
DR	DR	DR	PROSITE; PS50062; BCL2_FAMILY; 1.
DR	DR	DR	PROSITE; HGNC:959; BAX.
DR	DR	DR	MIM: 600040; -.
DR	DR	DR	InterPro; IPR002475; BCL2_family.
DR	DR	DR	InterPro; IPR000712; Bcl2_BH.
DR	DR	DR	Pfam; PF00412; Bcl-2; 1.
DR	DR	DR	SMART; SM00337; BCL; 1.
DR	DR	DR	PROSITE; PS01080; BHL; 1.
DR	DR	DR	PROSITE; PS01258; BH2; 1.
DR	DR	DR	PROSITE; PS01259; BH3; 1.
DR	DR	DR	PROSITE; PS50062; BCL2_FAMILY; 1.
KW	KW	DR	Apoptosis; Anti-oncogene; Transmembrane; Alternative splicing; Disease mutation.
FT	DOMAIN	DR	FT DOMAIN 59 73 BH3.
FT	DOMAIN	DR	FT DOMAIN 98 118 BHL.
FT	TRANSMEM	DR	FT TRANSMEM 150 165 BH2.
FT	VARIANT	DR	FT VARIANT 172 192 POTENTIAL.
FT	VARIANT	DR	G->R (IN T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA; LOSS OF HETERO DIMERIZATION WITH BCL-2 OR BCL-X(L)).
FT	VARIANT	DR	/FTid=VAR_01375.
FT	VARIANT	DR	G->R (IN T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA; LOSS OF HETERO DIMERIZATION).
FT	VARIANT	DR	G->V (IN BURKITT LYMPHOMA; LOSS OF HETERO DIMERIZATION).
FT	VARIANT	DR	/FTid=VAR_013576.
SQ	SEQUENCE	DR	SEQUENCE 192 AA; 21184 MW; 650CDB0A7DEBA994 CRC64;
CC	Query Match	DR	85.9%; Score 67; DB 1; Length 192;
CC	Best Local Similarity	DR	73.7%; Pred. No. 1.4e-05;
CC	Matches	DR	0; Mismatches 5; Indels 0; Gaps 0;
CC	Query Match	DR	85.9%; Score 67; DB 1; Length 218;
CC	Best Local Similarity	DR	73.7%; Pred. No. 1.6e-05;
CC	Matches	DR	0; Mismatches 5; Indels 0; Gaps 0;

XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Johnson EM, Easton R;
 XX
 DR WIL; 2000-339513;29.
 XX
 PT truncated BAX polypeptides useful for preventing apoptosis of neurons
 PR for the treatment of nervous system disorders -
 XX
 PS Disclosure; Page 35-36; 43pp; English.
 XX
 CC The present sequence is a human BAX alpha protein, a pro-apoptotic
 peptide which is a member of BCL-2 family of proteins that are involved
 in regulation of neuronal programmed cell death. The patent discloses
 specific truncated proteins derived from BAX alpha which inhibit neuronal
 apoptosis induced by trophic factor deprivation. The anti-apoptotic
 truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
 These proteins contain the N-terminal region, and at least a portion of
 the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
 transmembrane domains. The tBAX protein lacking only the
 CC spinal cord injury, head trauma and stroke.
 CC The tBAX proteins are used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC especially conditions chosen from neoplasias, diseases caused by
 CC Epstein Barr virus, African swine fever virus and adenovirus,
 CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
 CC inflammation and autoimmune disease or a condition mediated by
 CC excessive apoptosis, especially immunodeficiency diseases, senescence,
 CC neurodegenerative disease, ischemic and reperfusion cell death,
 CC infertility and wounds. The methods can also be used to identify
 CC apoptosis-modulating compounds.

SQ Sequence 192 AA:

Query Match 100.0%; Score 106; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1 6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCGEOPRGGGPTSSQIM 20
 Db 1 MGCGEOPRGGGPTSSQIM 20

RESULT 13

AYA69202 AAY69202 standard; peptide: 192 AA.

XX
 AC AAY69202;

XX
 DT 30-MAY-2000 (first entry)

DE Amino acid sequence of the human Bax protein.

XX
 KW pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;

KW cytochrome C transport; mitochondria; apoptosis; ion selectivity;

KW anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus;

KW African swine fever virus; adenovirus; lymphoproliferative condition;

KW cancer; arthritis; Crohn's disease; inflammation; autoimmune disease;

KW immunodeficiency; senescence; neurodegenerative disease;

KW reperfusion cell death; infertility; wound.

XX
 OS Homo sapiens.

XX
 PN WO200006187-A2.

PD 10-FEB-2000.

XX
 PF 30-JUL-1999; 99WO-US17276.

XX
 PR 31-JUL-1998; 98US-0127048.

XX
 PA (UNIW) UNIV WASHINGTON.

XX
 PI Korsmeyer SJ, Schlesinger PH;

XX
 DR WPI; 2000-195193;17.

PT Modulating apoptosis in cells by modulating channel ion selectivity for

PT transport of cytochrome C -

XX
 PS Disclosure; Page 34; 57pp; English.
 XX
 CC The present sequence represents the Bax protein. A pro-apoptotic
 peptide can be derived from the BH3 domain. The peptide is an inducer
 CC of formation of a channel for transport of cytochrome C out of
 CC mitochondria. The peptide induces apoptosis in a cell. The peptide
 CC changes the ion selectivity of an anti-apoptotic BCL-2 family member
 CC from potassium selective to chloride selective. The specification
 CC also describes inhibitors of apoptosis in cells. The inhibitors and
 CC inducers can be used to treat patients, preferably humans with a
 CC condition mediated by excessive down-regulation of apoptosis,
 especially conditions chosen from neoplasias, diseases caused by
 CC Epstein Barr virus, African swine fever virus and adenovirus,
 CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
 CC inflammation and autoimmune disease or a condition mediated by
 CC excessive apoptosis, especially immunodeficiency diseases, senescence,
 CC neurodegenerative disease, ischemic and reperfusion cell death,
 CC infertility and wounds. The methods can also be used to identify
 CC apoptosis-modulating compounds.

SQ Sequence 192 AA:

Query Match 100.0%; Score 106; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1 6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCGEOPRGGGPTSSQIM 20
 Db 1 MGCGEOPRGGGPTSSQIM 20

RESULT 14

AAB74121 AAB74121 standard; Protein: 192 AA.

XX
 AC AAB74121;

XX
 DT 22-MAY-2001 (first entry)

DE Human bcl-2 associated X protein (Bax) #1.

XX
 KW Human; Bax; cytostatic; immunosuppressive; immunostimulant; infection;

KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;

KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

KW myocardial infarction; traumatic brain injury; ischaemia;

KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

KW lymphoproliferative disease.

XX
 OS Homo sapiens.

XX
 PN US6184202-B1.

XX
 PD 05-FEB-2001.

XX
 PF 11-SEP-1997; 97US-0927326.

XX
 PR 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

XX
 PA (UNIW) UNIV WASHINGTON.

XX
 PI Korsmeyer SJ;

XX
 DR WPT; 2001-256104/26.

XX
 PT N-PSDB; AAF7704.

PT Modulating apoptosis of a cell, useful in maintaining homeostasis in

PT adult tissues, or treating proliferative or autoimmune diseases,

PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd

PT bcl-2 associated X protein -

QY 1 MDGSGEQPRGGGTTSSEQIM 20
 |||||||
 ID AAY34150 standard; Protein: 192 AA.
 XX
 AC AAY34150;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human wild-type Bax protein.
 XX
 KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX

QY 1 MDGSGEQPRGGGTTSSEQIM 20
 |||||||
 ID AAY05435 standard; peptide: 192 AA.
 XX
 AC AAY05435;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX protein sequence.
 XX
 KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.
 KW
 OS Homo sapiens.
 XX
 PN WO9946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 99WO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077541.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Roth JA;
 XX
 DR WPI: 1999-551404/46.
 DR N PSDB; AAZ19764.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 XX
 PS Disclosure; Page 149-150; 151pp; English.
 XX

This sequence represents human wild-type Bax protein. A naturally occurring mutant protein (AAV34149) was also isolated. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the expression of Bax is upregulated at the transcriptional level by p53, and Bax mRNA and protein expression have been shown to increase following induction of p53. Bax protein can function as a homodimer, or it can heterodimerize with other Bcl-2 gene family members such as the antiapoptotic protein Bcl-2. Heterodimerization of Bcl-2 family members provides a means of controlling cell death via the "rheostat" model. This model suggests that the relative amounts of Bcl-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing the Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.

XX Sequence 192 AA;

Query Match 100.0%; Score 106; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGTTSSEQIM 20
 |||||||
 ID AAY05435 standard; peptide: 192 AA.
 XX
 AC AAY05435;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX protein sequence.
 XX
 KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.
 KW
 OS Homo sapiens.
 XX
 PN WO9916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 98WO-US19765.
 XX
 PR 07-OCT-1997; 97US-0346039.
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-255058/21.
 XX
 PT Bcl homology domain 3 polypeptide
 XX
 PS Disclosure; Fig 21c; 104pp; English.
 XX

This sequence represents the human BAX protein. The invention relates to a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell, a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death regulation.

SQ Sequence 192 AA;

Query Match 100.0%; Score 106; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGTTSSEQIM 20

Db 1 MDGSGEQPRGGGTTSSEQIM 20

RESULT 10
 AAW87804
 AC AAW87804;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE A human Bcl-2 associated protein designated Bax.

AAV34149
ID AAV34149 standard; Protein: 131 AA.
XX
AC AAV34149;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human truncated Bax protein.
XX
KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 59..101 /note= "Portion of BH3 domain essential for dimerisation"
FT
XX
PN WO946371-A2.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05359.
XX
PR 11-MAR-1998; 98US-0077541.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
PI Ji L, Roth JA;
XX
WPT; 1999-551404/16.
DR N-PSDB; ARZ19763.
XX
PT New adenovirus vectors used for killing or inhibiting the growth of
PT cells and for treating cancers -
XX
PS Claim 26; Page 148-149; 151pp; English.
XX
CC This sequence represents a human truncated Bax protein. The cDNA
CC contains a single base deletion relative to the wild-type (AAZ19764),
CC causing a frameshift which leads to translation of a premature stop
CC codon, resulting in a truncated protein. However, the domain responsible
CC for its function is still present in the truncated protein. Bax (Bcl-2
CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
CC Bax functions as a primary response gene in the p53-regulated apoptotic
CC pathway. The Bax gene promoter has 4 p53 binding sites and the
CC expression of Bax is upregulated at the transcriptional level by p53, and
CC Bax mRNA and protein expression have been shown to increase following
CC induction of p53. Bax protein can function as a homodimer, or it can
CC heterodimerise with other Bcl-2 gene family members such as the
CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
CC provides a means of controlling cell death via the "rheostat" model. This
CC model suggests that the relative amounts of Bcl-2 and Bax determine the
CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
CC in excess, however, Bax homodimers predominate and the cell becomes
CC susceptible to apoptosis following exposure to an apoptotic stimulus.
CC Additionally, Bax can function in its monomeric form to accelerate cell
CC death. Use of novel adenoviral vectors containing this Bax gene may
CC augment and complement wild type p53 gene therapy, which induces a G1
CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
CC mutations. In addition, Bax overexpression could provide the apoptotic
CC effect of p53 without the need for p53 itself.
XX
SQ Sequence 131 AA;

Query Matchⁿ 100.0%; Score 106; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 1; le-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPDSGEQPRGGGTSSEQIM 20
Db 1 MDGSGEQPRGGGTSSEQIM 20

RESULT 7
ID AAR71406
XX
AC AAR71406
XX
DT 15-NOV-1995 (first entry)
XX
DE Human Bax protein.
XX
KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
KW proliferation; cell cycle progression; Bax; apoptotic cell death;
KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
KW ischaemic cell death.

XX
OS Homo sapiens.
XX
PN WO9505750-A.
XX
PD 02-MAR-1995.
XX
PA 24-AUG-1994; 94WO-US09701.
XX
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR N-PSDB; AAQ97606.
XX
PT Methods for producing and identifying mutant bcl-2 Proteins -
PT that lack death repressor activity and/or lacks binding to Bax.
XX
PS Disclosure; Fig 3; 133PP; English.
XX
CC This sequence represents human Bax protein. Bax is a protein which is
CC associated with the human bcl-2 alpha and beta proteins, the sequences
CC of which are given in AAR71404-05 respectively. bcl-2 is encoded by a
CC proto-oncogene and is capable of inhibiting apoptosis in many
CC hematopoietic cell systems. bcl-2 is a 26 kd membrane-associated
CC cytoplasmic protein and is thought to function by enhancing the survival
CC of hematopoietic cells of B and T origins rather than directly promoting
CC proliferation of these cell types. bcl-2 has not been shown to directly
CC promote cell cycle progression nor does it necessarily alter the dose
CC response to limiting concentrations of IL-3. bcl-2 has been shown to
CC form heterodimers with this 21 kd protein, Bax. Overexpressed Bax
CC accelerates apoptotic cell death induced by cytokine deprivation in an
CC IL-3 dependent cell line, and it also acts to counter the death repressor
CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
CC cell survival or death following an apoptotic stimulus. The invention
CC gives a mutant form of bcl-2 in which there is at least one amino acid
CC substitution or deletion in the BH1 or BH2 domains. This makes the
CC mutant protein substantially incapable of binding Bax and/or incapable
CC of death repressor activity. Down regulation of bcl-2 is useful in
CC cancer therapy, controlling hyperplasias and eliminating self-reactive
CC clones in autoimmunity by favouring death effector molecules. Up
CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
CC cell death.

XX
SQ Sequence 192 AA;

Query Matchⁿ 100.0%; Score 106; DB 16; Length 192;
Best Local Similarity 100.0%; Pred. No. 1; 6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX The present invention describes a pure protein (P1) comprising a BAX
 CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 CC apoptosis. The polypeptides and methods from the present invention are
 useful for identifying compounds that modulate apoptosis which can then
 be used for treating cancer. The present sequence represents a human
 CC BAX peptide sequence of amino acids 1 to 20, which is used in an
 CC example from the present invention.

XX Sequence 20 AA:

Query Match 100.0%; Score 106; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1 5e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGGmPSSEQIM 20
 Db 1 MDGSGEQPRGGGmPSSEQIM 20

RESULT 2
 AAV70816 standard; Protein: 70 AA.

ID AAV70816;
 XX
 AC AAV70816;
 XX
 DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein, tBAX70.

XX Human; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.

XX DE Human neuroprotective truncated BAX protein tBAX70 mutant.

XX Human; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH Region 1..58

FT /note= "N-terminal region of BAX alpha"

FT Domain 59..70

FT /label= "Partial BH3 domain
 /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"

FT /note= "Wild type Ser is substituted by Ala"

XX PN WO200023083-A1.

XX PD 27-APR-2000.

XX PF 22-OCT-1999; 99WO-US24747.

XX PR 22-OCT-1998; 98US-0177315.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Johnson EM, Easton R;

XX DR WPI; 2000-339513/29.

XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -

XX Claim 4: Page 32; 43pp; English.

XX PS The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX70 which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of the C-terminal transmembrane domain of human BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length
 CC BAX alpha, that includes the N-terminal region and a portion of the BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

The present sequence is used to treat diseases associated with neuronal

CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

XX Sequence 70 AA:

Query Match 100.0%; Score 106; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5 6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGGmPSSEQIM 20
 Db 1 MDGSGEQPRGGGmPSSEQIM 20

RESULT 3
 AAV70820 standard; Protein: 70 AA.

ID AAV70820;
 XX
 AC AAV70820;
 XX
 DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein tBAX70 mutant.

XX Human; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.

XX OS Synthetic.

XX Key Location/Qualifiers

FH Region 1..58

FT /note= "N-terminal region from BAX alpha"

FT Domain 59..70

FT /label= "Partial BH3 domain
 /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"

FT Misc-difference 55

FT Misc-difference 60

FT /note= "Wild type Ser is substituted by Ala"

XX PN WO200023083-A1.

XX PD 27-APR-2000.

XX PF 22-OCT-1999; 99WO-US24747.

XX PR 22-OCT-1998; 98US-0177315.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Johnson EM, Easton R;

XX DR WPI; 2000-339513/29.

XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -

XX Claim 4: Page 33-34; 43pp; English.

XX PS The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX70 mutant (tBAX70M), which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of the C-terminal transmembrane domain of human BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length
 CC BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:24:47 ; Search time 31.7949 Seconds

(without alignments)
83.819 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106

Sequence: 1 MDGSGEQPRGGPPISSQIM 20

Scoring table: BL0STM62

Gapop 10.0 , Gabext 0.5

Searched:

908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

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2: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1988.DAT:*

9: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1990.DAT:*

10: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1991.DAT:*

11: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1992.DAT:*

12: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1993.DAT:*

13: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1994.DAT:*

14: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1995.DAT:*

15: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1996.DAT:*

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17: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1998.DAT:*

18: /SIDS2/gcadata/geneseq/geneseq-emb1/AA1999.DAT:*

19: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2000.DAT:*

20: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2001.DAT:*

21: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT:*

22: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2003.DAT:*

23: /SIDS2/gcadata/geneseq/geneseq-emb1/AA2004.DAT:*

RESULT 1		ALIGNMENTS	
ID	AAV90736	standard; peptide;	20 AA.
XX			
AC	AAV90736;		
XX			
DT	17-AUG-2000	(first entry)	
XX			
DE	Human BAX amino acid sequence 1 to 20 SEQ ID NO:2.		
XX			
KW	Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis; cell death; cancer; cytostatic.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200020446-A2.		
XX			
PD	13-APR-2000.		
XX			
PF	05-OCT-1999; 99WO-1B01680.		
XX			
PR	05-OCT-1998; 98US-0166028.		
XX			
PA	(UVMC-) UNIV MCGILL.		
XX			
PI	Shore GC, Goping S;		
XX			
DR	WPI; 2000-303740/26.		
XX			
PT	BAX polypeptide lacking an ART domain, useful for identifying agents that modulate apoptosis which can then be used for treating cancer -		
XX			
PS	Example 2; Page 52; 53pp; English.		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	21	AAV90736 Human BAX amino acid
2	106	100.0	70	21	AAV70816 Human neuroprotective protein
3	106	100.0	70	21	AAV70820 Human neuroprotective protein
4	106	100.0	78	21	AAV70818 Human neuroprotective protein
5	106	100.0	78	21	AAV70822 Human neuroprotective protein
6	106	100.0	131	20	AAV34149 Human truncated Bax protein.
7	106	100.0	192	16	AAV71406 Human Bax protein.
8	106	100.0	192	15	AAV34150 Human wild-type Bax protein
9	106	100.0	192	20	AAV05435 Human Bax protein
10	106	100.0	192	20	AABW87804 A human Bcl-2 asso

FILE REFERENCE: ELTRA_011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3425
LENGTH: 322
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5425

Query Match 38.7%; Score 41; DB 10; Length 322;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 5 GEDPRGGPMSSEOM 20
| ||| || : :::::
Db 250 GHVORGGSPTGADRLV 265

Search completed: January 7, 2003, 12:37:21
Job time : 7.69231 secs

Sequence 2, Application US/09854093
 Patent No. US20020151698A1
 GENERAL INFORMATION:
 APPLICANT: Lester, Henry A.
 Dascal, Nathan
 Lin, Nancy
 Schreibmayer, Wolfgang
 Davidson, No. US20020151698A1man
 TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER G-PROTEIN ACTIVATED, MAMMALIAN POTASSIUM K_A CHANNEL AND USES THEREOF
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flent Rohbach Test Albritton & Herbert LLP
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/854,093
 FILING DATE: 10-May-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION NUMBER: 08/904,234
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Vance, Dolly A.
 REGISTRATION NUMBER: 39,054
 REFERENCE/DOCKET NUMBER: A-59891-1/RFT/DAV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 501 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-854-093-2

Query Match 39.6%; Score 42; DB 10; Length 501;
 Best Local Similarity 44.4%; Pred. No. 1.5e+02; Matches 8; Conservatve 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 3 GSSEQPRGGPSSSEQIM 20
 Db 21 GSGLQPOQPGQGPOQQLV 38

RESULT 14
 US-09-864-761-45406
 ; Sequence 44406, Application US/09864761
 ; Patent No. US2002008763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Starron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeromica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04

Query Match 38.7%; Score 41; DB 10; Length 24;
 Best Local Similarity 58.3%; Pred. No. 10; Matches 7; Conservatve 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MDGSQEPRGG 12
 Db 13 VEGSGEPVKGG 24

RESULT 15
 US-09-815-242-5425
 ; Sequence 5425, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes

Query Match 41.5%; Score 44; DB 10; Length 41;
 Best Local Similarity 47.1%; Pred. No. 6.9;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Query Match 40.6%; Score 43; DB 9; Length 534;
 Best Local Similarity 61.5%; Pred. No. 1.2e+02;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DGSGEOPRGPPSSEQ 18
 Db 4 DGESEEEGGGGKKEEE 20

RESULT 10
 US-10-058-820-5

; Sequence 5, Application US/10058820
 ; Patent No. US200215479A1

; GENERAL INFORMATION:
 ; APPLICANT: Bogen, Jonathan S.
 ; APPLICANT: Lodish, Harvey F.
 ; TITLE OF INVENTION: Expression Cloning Method

FILE REFERENCE: 0399 2025-002
 CURRENT APPLICATION NUMBER: US/10/058, 820
 CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/325, 651
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: US 60/298, 963
 PRIOR FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 60/264, 816
 PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 441
 TYPE: PRT
 ORGANISM: Mus musculus

Query Match 41.5%; Score 44; DB 9; Length 441;
 Best Local Similarity 57.1%; Pred. No. 73;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 EQRPGGGPNSSEQ 19
 Db 66 KQPARGGPQSQDSI 79

RESULT 11
 US-09-738-626-5681

; Sequence 5681, Application US/09738626
 ; Publication No. US200219605A1

; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738, 626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/15912
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 5681
 ; LENGTH: 534

Query Match 39.6%; Score 42; DB 10; Length 501;
 Best Local Similarity 44.4%; Pred. No. 1.5e+02;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GSGIOPRGGPTSSEQIM 20
 Db 21 GSGIOPQGQGQQQLV 38

RESULT 13
 US-09-854-093-2

US-09-925-301-1634

Query Match 42.5%; Score 45; DB 10; Length 88;
 Best Local Similarity 57.1%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT US-09-915-299-911

Sequence 911, Application US/09925299
 Patent No. US20020055627A1

GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: P102
 CURRENT APPLICATION NUMBER: US/09/925, 299
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05883
 PRIOR FILING DATE: 2000-01-08
 PRIOR APPLICATION NUMBER: 60/124, 270
 PRIOR FILING DATE: 1999-01-12
 NUMBER OF SEQ ID NOS: 155
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 911
 LENGTH: 1242
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (224)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (1013)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (1034)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

RESULT 9

Query Match 42.5%; Score 45; DB 10; Length 1242;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT US-09-925-299-911

Sequence 1097, Application US/09119855
 Patent No. US20020059197A1

GENERAL INFORMATION:
 APPLICANT: Curtis, Rory A.J.
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 FILE REFERENCE: mini_055
 CURRENT APPLICATION NUMBER: US/09/119,855
 NUMBER OF SEQ ID NOS: 13
 CURRENT FILING DATE: 1998-07-21
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 1284
 TYPE: PRT
 ORGANISM: Drosophila melanogaster

RESULT 8

Query Match 42.5%; Score 45; DB 10; Length 1242;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT US-09-119-855-11

Sequence 1097, Application US/09119855
 Patent No. US20020059197A1

GENERAL INFORMATION:
 APPLICANT: Curtis, Rory A.J.
 TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 FILE REFERENCE: mini_055
 CURRENT APPLICATION NUMBER: US/09/119,855
 NUMBER OF SEQ ID NOS: 13
 CURRENT FILING DATE: 1998-07-21
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 1284
 TYPE: PRT
 ORGANISM: Drosophila melanogaster

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

RESULT 9

Query Match 42.5%; Score 45; DB 15; Length 75;
 Best Local Similarity 61.5%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

RESULT 9

Query Match 42.5%; Score 45; DB 10; Length 1284;
 Best Local Similarity 61.5%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

RESULT 9

Query Match 42.5%; Score 45; DB 10; Length 1284;
 Best Local Similarity 61.5%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

RESULT 9

Query Match 42.5%; Score 45; DB 10; Length 1284;
 Best Local Similarity 61.5%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

RESULT 9

Query Match 42.5%; Score 45; DB 10; Length 1284;
 Best Local Similarity 61.5%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT US-09-864-761-38626

Sequence 1097, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Haenzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
FILE REFERENCE: 9457-009-999
CURRENT APPLICATION NUMBER: US/09/033, 525
CURRENT FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-033-525-2

RESULT 3
Query Match 97.2%; Score 103; DB 10; Length 331;
Best Local Similarity 95.0%; Pred. No. 8.5e-07; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 0;
QY 1 MDGSGEQOPRGGGTSSSEQIM 20
Db 140 MDGSGEQOPRGGGTSSSEQIM 159

RESULT 4
US-09-876-204-4
Sequence 4, Application US/09876204
Patent No. US2002005316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/01001
CURRENT APPLICATION NUMBER: US/09/876, 204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/166, 028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 20
TYPE: PRT
ORGANISM: Mus musculus
US-09-876-204-4

Query Match 78.3%; Score 83; DB 10; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.3e-05; Indels 3; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;
QY 1 MDGSGEQOPRGGGTSSSEQIM 20
Db 1 MDGSGEQOPRGGGTSSSEQIM 20

RESULT 4
US-09-876-204-5
Sequence 5, Application US/09876204
Patent No. US2002005316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/01001
CURRENT APPLICATION NUMBER: US/09/876, 204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/166, 028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-876-204-5

Query Match 76.4%; Score 81; DB 10; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.2e-05;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDGSGEQOPRGGGTSSSEQIM 20
Db 1 MDGSGDHGGGTSSSEQIM 20

RESULT 5
US-09-876-204-1
Sequence 1, Application US/09876204
Patent No. US2002005316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/01001
CURRENT APPLICATION NUMBER: US/09/876, 204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/166, 028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic based on consensus sequence of Homo sapiens, Mus musculus, and Rattus norvegicus
NAME/KEY: VARIANT
LOCATION: (6)..(10)
OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1

Query Match 63.2%; Score 67; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.0029; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 5;
QY 1 MDGSGEQOPRGGGTSSSEQIM 19
Db 1 MDGSGXXXXGGTSSSEQIM 19

RESULT 6
US-09-925-301-1634
Sequence 1634, Application US/09925301
Patent No. US2002005308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925, 301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124, 270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1634
LENGTH: 88
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (88)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Om protein - protein search, using sw model

Run on: January 7, 2003, 12:30:53 ; Search time 7.69231 Seconds
 (without alignments)
 49.274 Million cell updates/sec

Title: US-09-876-204-3
 Perfect score: 106
 Sequence: 1 MDGSGEQPRGGPSSSEQIWM 20

Scoring table: BLASTM62
 Gapext 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA,*

1: /cgn2_6/ptodata/1/pubbaa/US08_NEW_PUB_pep:*

2: /cgn2_6/ptodata/1/pubbaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubbaa/US06_NEW_PUB_pep:*

4: /cgn2_6/ptodata/1/pubbaa/US05_PUB_pep:*

5: /cgn2_6/ptodata/1/pubbaa/US07_NEW_PUB_pep:*

6: /cgn2_6/ptodata/1/pubbaa/US07_PUBCOMB_pep:*

7: /cgn2_6/ptodata/1/pubbaa/PCTUS_PUBCOMB_pep:*

8: /cgn2_6/ptodata/1/pubbaa/US08_PUBCOMB_pep:*

9: /cgn2_6/ptodata/1/pubbaa/US09_NEW_PUB_pep:*

10: /cgn2_6/ptodata/1/pubbaa/US09_PUBCOMB_pep:*

11: /cgn2_6/ptodata/1/pubbaa/US10_NEW_PUB_pep:*

12: /cgn2_6/ptodata/1/pubbaa/US10_PUBCOMB_pep:*

13: /cgn2_6/ptodata/1/pubbaa/US60_NEW_PUB_pep:*

14: /cgn2_6/ptodata/1/pubbaa/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	106	100.0	20	10 US-09-876-204-3
2	103	97.2	331	10 US-09-876-204-3
3	83	78.3	20	10 US-09-876-204-4
4	81	76.4	20	10 US-09-876-204-5
5	67	63.2	19	10 US-09-876-204-1
6	45	42.5	88	10 US-09-945-301-1634
7	45	42.5	1242	10 US-09-935-299-911
8	45	42.5	1284	10 US-09-919-855-11
9	44	41.5	41	10 US-09-884-761-38626
10	44	41.5	441	9 US-10-058-820-5
11	43	38.7	322	10 US-09-815-241-5425
12	42	39.6	501	10 US-09-039-927A-2
13	42	39.6	501	10 US-09-854-093-2
14	41	38.7	24	10 US-09-664-661-506
15	41	38.7	322	10 US-09-815-242-12619
16	41	38.7	322	10 US-09-815-242-12619
17	41	38.7	322	10 US-09-815-242-12619
18	41	38.7	351	10 US-09-350-874-61
19	38.7	351	10	US-09-801-368-184

RESULT 1
 US-09-876-204-3
 ; Sequence 3, Application US/09876204
 ; Patent No. US20020052316A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gordon C. Shore et al.
 ; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
 ; FILE REFERENCE: 50013/011001
 ; CURRENT APPLICATION NUMBER: US/09/876, 204
 ; CURRENT FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 09/166, 028
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-876-204-3

Query Match Best Local Similarity 100.0%; Score 106; DB 10; Length 20;
 Matches 20; Conservative 100.0%; Pred. No. 2.1e-08; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGPSSSEQIWM 20
 Db 1 MDGSGEQPRGGPSSSEQIWM 20

RESULT 2
 US-09-033-525-2
 ; Sequence 2, Application US/09033525
 ; Patent No. US20020090374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yarkoni, Shai
 ; APPLICANT: Ben Rehida, Ahmi
 ; APPLICANT: Azar, Yehudit
 ; APPLICANT: Agrelian, Ram
 ; APPLICANT: Belotsotsky, Ruth
 ; APPLICANT: Loberbaum-Galski, Haya
 ; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING

FT ECOR40, ECOR49, ECOR50 ABD ECOR65)

Job time : 9.30769 secs

SQ	SEQUENCE	618 AA;	67233 MW;	EBB551C3E2946AC3	CRC64:
Query Match		47.4%	Score 37;	DB 1;	Length 618;
Best Local Similarity		42.1%	Pred. No. 25;		
Matches	8;	Conservative	Mismatches	9;	Indels 0;
Qy	1	MDGSXXXXKGPTSSQI	19		Gaps 0
		:			
Db	338	MDGEETQGNTGGDTTAQOI	356		

RESULT 15			
HS73_BOVIN		STANDARD; PRT; 631 AA.	
ID	HS73_BOVIN		
P34933;			
DT	01-FEB-1994 (Rel. 28; Created)		
DT	15-FEB-1994 (Rel. 28; Last sequence update)		
DT	15-DEC-1998 (Rel. 37; Last annotation update)		
DE	Heat shock 70 kDa protein 3.		
GN	HSP70-3.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.		
OX	NCBI_TAXID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE#93122795; PubMed#1478667;		
RA	GROZ M.D., WOMACK J.E., SKOW L.C.;		
RT	"Syntetic conservation of HSP70 genes in cattle and humans.";		
RL	Genomics 14:863-868;1992.		
CC	-!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION OR FOLLOWING STRESS-INDUCED DAMAGE.		
CC	-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaborative		

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CC modified and this statement is not removed. It may be used for commercial
CC purposes if the source is cited.

SO SEQUENCE 631 AA; 63199 MW; 01ACA20600C5322F CRC64;
Query Match 47.4%; Score 37; DB 1; Length 631;

Best Local Similarity 46.7%; Pred. No. 26; Mismatches 0; Indels 8; Gaps 0

Search completed: January 7, 2003, 12:29:50

CC or send an email to license@isb-sib.ch).

RN [3]
RN SEQUENCE FROM N.A.
RP
RC STRAIN-K12;
RX MEDLINE-97251357; PubMed=9097039;
DR SGD; S0001747; GAB1.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004840; AAC_permease.
DR InterPro; IPR004341; permease.
DR InterPro; IPR004762; Yeast_AA_perm.
DR Pfam; PF00324; aa_permeases_1.
DR TIGRFAMS; TIGR00913; 2A0310_1.
DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 96 116 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 166 185 POTENTIAL.
FT TRANSMEM 205 224 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT TRANSMEM 281 298 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 377 396 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 530 548 POTENTIAL.
FT TRANSMEM 530 548 MISSING (IN REF. 1).
FT CONFLICT 122 122 S -> A (IN REF. 1).
FT CONFLICT 189 189 I -> V (IN REF. 1).
FT CONFLICT 338 338 V -> L (IN REF. 1).
FT CONFLICT 518 518 SEQUENCE 602 AA; 65655 MW; 5363616647907458 CRC64;
SQ Query Match 47.4%; Score 37; DB 1; Length 602;
Best Local Similarity 53.8%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0; CC
OQ 3 GSXXXXXGGPVS 15
DB 111 GSCTALRTGGPAS 123

RESULT 14

SPPA_ECOLI STANDARD; PRN; 618 AA.
ID P08395; P77752; Q46723; Q46724; Q46725; Q46726; Q57183;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE protease IV (EC 3.4.21.-) (Endopeptidase IV) (signal peptide
peptidase)
GN SPPA OR Bl766.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TAXID=562;
RN [1]
RN SEQUENCE FROM N.A.;|
RX MEDLINE-86220892; PubMed=3522590;
RA Ichihara S., Suzuki T., Suzuki M., Mizushima S.,
RT "Molecular cloning and sequencing of the SPPA gene and
characterization of the encoded protease IV, a signal peptide
peptidase, of Escherichia coli";
J. Biol. Chem. 261:9405-9411(1986).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mai B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [3]
RN SEQUENCE FROM N.A.
RP
RC STRAIN-K12;
RX MEDLINE-97251357; PubMed=9097039;
DR SGD; S0001747; GAB1.
RA Makino K., Miki T., Mizobuchi K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Baba T., Fujita K., Kitakawa M., Kitagawa M.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map";
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQQUENCE OF 110-433 FROM N.A.
RC STRAIN-Various ECOR strains;
RX MEDLINE-95054015; PubMed=7573728;
RA Guttmann D.S.; Dykhuizen D.E.;
RT "Clonal divergence in Escherichia coli as a result of recombination,
not mutation";
Science 266:1380-1383(1994).
CC FUNCTION DIGESTION OF THE CLEAVED SIGNAL PEPTIDES. THIS ACTIVITY
IS NECESSARY TO MAINTAIN PROPER SECRETION OF MATURE PROTEINS
CC ACROSS THE MEMBRANE.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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--
CC DR EMBL; M13359; AAA24648.1; .
CC DR EMBL; AB000271; AAC74836.1; .
CC DR EMBL; B90820; BAA1557.1; .
CC DR EMBL; U13772; AAH5708.1; .
CC DR EMBL; U13773; AAH5709.1; .
CC DR EMBL; U13774; AAH57010.1; .
CC DR EMBL; U13775; AAH57011.1; .
CC DR EMBL; U13776; AAH57012.1; .
CC DR EMBL; U13777; AAH57013.1; .
CC DR EMBL; U13778; AAH57014.1; .
CC DR EMBL; U13779; AAH57015.1; .
CC DR EMBL; U13780; AAH57016.1; .
CC DR EMBL; U13782; AAH57017.1; .
CC DR EMBL; U13833; AAH57030.1; .
CC DR EMBL; U13834; AAH57031.1; .
CC DR PIR; A24813; PRECT4.
CC DR MEROPS; S49_001; .
CC DR Ecogene; EG10968; SPPA.
CC DR InterPro; IPR02142; Peptidase_U7.
CC DR InterPro; IPR004335; Signprote_SPPA36.
CC DR InterPro; IPR004634; Signprote_SPPA67.
CC DR Pfam; PF01343; Peptidase_U7; 2.
CC DR PRODOM; PD002897; Peptidase_U7; 1.
CC DR TIGRFAMS; TIGR00705; SPPA_67K; 1.
CC DR TIGRFAMS; TIGR00706; SPPA_dom; 1.
CC KW Hydrolase; Protease; Transmembrane; Inner membrane; Complete proteome.
CC FT TRANSMEM 29 45 POTENTIAL.
CC FT TRANSMEM 398 41 POTENTIAL.
CC FT VARIANT 421 441 POTENTIAL.
CC FT VARIANT 151 151 V -> I (IN STRAINS ECOR49 AND ECOR50).
CC FT VARIANT 186 185 G -> S (IN STRAIN ECOR16).
CC FT VARIANT 252 252 E -> H (IN STRAIN ECOR16).
CC FT VARIANT 252 252 E -> K (IN STRAIN ECOR49).
CC FT VARIANT 252 252 E -> O (IN STRAINS ECOR38, ECOR39, ECOR40, ECOR50, ECOR65 AND ECOR68).
CC FT VARIANT 294 294 A -> T (IN STRAINS ECOR38, ECOR39).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC
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 CC
 DR EMBL; AL356012; CAB91572_1; -.
 DR InterPro; IPR002293; AAC:rel_permeasel.
 DR InterPro; IPR004840; AAC_permease.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa_permeases; 1.
 DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane.
 FT TRANSMEM 109 129 POTENTIAL.
 FT TRANSMEM 188 208 POTENTIAL.
 FT TRANSMEM 216 236 POTENTIAL.
 FT TRANSMEM 304 324 POTENTIAL.
 FT TRANSMEM 348 368 POTENTIAL.
 FT TRANSMEM 402 422 POTENTIAL.
 FT TRANSMEM 472 492 POTENTIAL.
 FT TRANSMEM 514 534 POTENTIAL.
 SQ SEQUENCE 579 AA; 63259 MW; C60DF4BEB4397CD3 CRC64;
 Query Match 47.4%; Score 37; DB 1; Length 579;
 Best Local Similarity 53.8%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 3 GSGXXXXGGPTS 15
 Db 98 GSGSALADGCPAS 110

RESULT 13	
ID	NAME
GAP1_YEAST	STANDARD;
P19145;	PRT;
DT 01-JUN-1994	DB 1;
DT 01-NOV-1997	Length 579;
DE General amino acid permease GAP1.	
GN GAPI OR YKR039W.	
OS Saccharomyces cerevisiae (Baker's yeast).	
OC Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC Sacccharomycetales; Sacccharomycetaceae; Sacccharomyces.	
OX NCBI_TaxID=4932;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE-90306009; PubMed=2194797;	
RA Jauniaux J.-C., Grenon M.	
RT "GAPI", the general amino acid permease gene of <i>Saccharomyces</i>	
RT cerevisiae. Nucleotide sequence, protein similarity with the other	
RT bakers yeast amino acid permeases, and nitrogen catabolite	
RT repression.";	
RL Eur. J. Biochem. 190:39-44(1990).	
RN [2]	
RP SEQUENCE FROM N.A.	
RA Urrestarazu L.A., Jauniaux J.-C.;	
RL Submitted (MAR-1994) to the EMBL/genBank/DDJB databases.	
CC -!- FUNCTION: PERMEASE FOR VARIOUS AMINO ACIDS AS WELL AS FOR GABA.	
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.	
CC -!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.	
CC	
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or send an email to license@isb-sib.ch).	

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 MGSGCXXXXXGPTSSBOI 19
 ID ||||| ||||||| 19
 AC Q05941;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Heat shock 70 kDa protein.
 GN HSP70_1.
 OS Hydra magnipapillata (Hydra).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 OC Hydriidae; Hydra
 OX NCBI_TaxID=6085;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=93130891; PubMed=1483453;
 RA Gellman K., Praetzel G., Bosch T.C.G.;
 RT "Cloning and expression of a heat-inducible hsp70 gene in two species
 RT of Hydra which differ in their stress response.";
 RL Eur. J. Biochem. 210:683-691(1992).
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
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 CC
 DR EMBL; M84019; AAA29213.1; -.
 DR PIR; S27004; S27004.
 DR HSSP; P08109; ICKR.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70_1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 654 AA; 71467 MW; 5BC1EA4BAE640FB CRC64;
 Query Match 59.0%; Score 46; DB 1; Length 654;
 Best Local Similarity 52.9%; Pred. No. 0.51; Mismatches 9; Conservatism 0; Mismatches 8; Indels 0; Gaps 0;

RP SEQUENCE FROM N_A.
 Oy 1 MGSGCXXXXXGPTSS 17
 ID ||||| ||||||| 17
 DB 636 MGSGSKASSGGPTTE 652

RESULT 8

YGRM MICRO STANDARD; PRT; 105 AA.

ID YGRM MICRO
 AC P24621;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-FEB-1995 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in GRW 3' region (Fragment).
 OS Micromonospora rosea.
 OC Bacteria; Actinobacteria; Actinomycetales; Micromonosporineae; Micromonosporaceae;
 OC Micromonospora.
 OX NCBI_TaxID=1878;
 RN [1]

RP SEQUENCE FROM N_A.
 RX MEDLINE=91192615; PubMed=2013410;
 RA Klemens G.H., Cundliffe E., Finansek I.;
 RT "Cloning and characterization of gentamicin-resistance genes from
 RT Micromonospora purpurea and Micromonospora rosea.*";
 RL Gene 98:51-60 (1991).
 CC
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 or send an email to license@ist-sib.ch).
 CC
 DR EMBL; M5521; AAA25339.1; -.
 DR PIR; PW0018; PW0018.
 KW Antibiotic resistance; Hypothetical protein.
 FT NON_TER 105 105
 SQ SEQUENCE 105 AA; 11112 MW; 56125793440BA48C CRC64;

Query Match 50.0%; Score 39; DB 1; Length 105;
 Best Local Similarity 61.5%; Pred. No. 1.5; Mismatches 8; Conservatism 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 SGXXXXXGPTSS 16
 ID ||||| ||||||| 16
 DB 74 SGCVAAATGGPTSS 86

RESULT 9

PHP2_SCHPO STANDARD; PRT; 334 AA.

ID PHP2_SCHPO
 AC P24488;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DR 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transcriptional activator php2.
 DR PHP2 OR SPAC725_11C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetidae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;

RP SEQUENCE FROM N_A.
 RC STRAIN=401;
 RX MEDLINE=91117227; PubMed=1899284;
 RA Olesen J.T., Fikes J.D., Guarante L.;
 RT "The Schizosaccharomyces pombe homolog of Saccharomyces cerevisiae
 RT HAP2 reveals selective and stringent conservation of the small
 RT essential core protein domain.";
 RL Mol. Cell. Biol. 11:611-619(1991).
 RN [2]

RP SEQUENCE FROM N_A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sqorros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodges G.,
 RA Hollroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Munagala K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,



Sequence 161, Application US/09826290
 Patent No. US20020164668A1
 ; GENERAL INFORMATION;
 ;
 ; APPLICANT: Durham, L. Kathryn
 ; APPLICANT: Friedman, David L.
 ; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
 ; APPLICANT: Kimmel, Lida H.
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Potter, David M.
 ; APPLICANT: Rohlf, Christian
 ; APPLICANT: Silber, B. Michael
 ; APPLICANT: Stiger, Thomas R.
 ; APPLICANT: Sunderland, P. Trey
 ; APPLICANT: Townsend, Robert Reid
 ; APPLICANT: White, Frost
 ;
 APPLICANT: Williams, Stephen A.
 TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Treatment of
 TITLE OF INVENTION: Alzheimer's Disease
 FILE REFERENCE: 2572-1-001 N2
 CURRENT APPLICATION NUMBER: US/09/826,290
 CURRENT FILING DATE: 2001-04-30
 PRIOR APPLICATION NUMBER: US 60/194,504
 PRIOR FILING DATE: 2000-04-03
 PRIOR APPLICATION NUMBER: US 60/253,647
 PRIOR FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 492
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 161
 LENGTH: 14
 TYPE: PRT
 ORGANISM: homo sapien
 US-09-826-290-161

RESULT 15
 US-09-826-290-294
 ; Sequence 294, Application US/09826290
 ; Patent No. US20020164668A1
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Durham, L. Kathryn
 ; APPLICANT: Friedman, David L.
 ; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
 ; APPLICANT: Kimmel, Lida H.
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Potter, David M.
 ; APPLICANT: Rohlf, Christian
 ; APPLICANT: Silber, B. Michael
 ; APPLICANT: Stiger, Thomas R.
 ; APPLICANT: Sunderland, P. Trey
 ; APPLICANT: Townsend, Robert Reid
 ; APPLICANT: White, Frost
 ;
 APPLICANT: Williams, Stephen A.
 TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Treatment of
 TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
 TITLE OF INVENTION: Alzheimer's Disease
 FILE REFERENCE: 2572-1-001 N2
 CURRENT APPLICATION NUMBER: US/09/826,290
 CURRENT FILING DATE: 2001-04-30
 PRIOR APPLICATION NUMBER: US 60/194,504
 PRIOR FILING DATE: 2000-04-30
 PRIOR APPLICATION NUMBER: US 60/253,647
 PRIOR FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 492
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 161
 LENGTH: 14
 TYPE: PRT
 ORGANISM: homo sapien
 US-09-826-290-161

Query	Match	Score	DB	Length
Best Local Matches	5; Conservative	5;	30;	14;
Qy	2 DGSGE 6	0;	Mismatches	
Db	5 DGSGE 9	0;	Indels	
		0;	Gaps	

; SEQ ID NO 294
 ; LENGTH: 14
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: homo sapien
 US-09-826-290-294

Query	Match	Score	DB	Length
Best Local Matches	25.0%;	Score 5;	DB 9;	Length 14;
Current Application Number:	100.0%;	Pred. No. 30;		
Matches	5;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

Search completed: January 7, 2003, 12:46:23
 Job time : 7.69231 secs

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MC-DOS
 COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/850,048A
 FILING DATE: 07-May-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/609,187
 FILING DATE: 1996-03-01

ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 8389-028-999

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 730 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 30.0%; Score 6; DB 10; Length 730;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PRGGP 13
 Db 191 PRGGP 196

RESULT 11
 US-09-978-698-2
 Sequence 2, Application US/099788698
 Patent No. US2002015010A1

GENERAL INFORMATION:
 APPLICANT: Rayapati, P. John
 APPLICANT: Rayapati, Corey M.
 TITLE OF INVENTION: Regulation of Carbon Assimilation

FILE REFERENCE: 1533.093001
 CURRENT APPLICATION NUMBER: US/09/978,698
 CURRENT FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: 09/606,312
 PRIOR FILING DATE: 2000-06-29
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 966
 TYPE: PRT
 ORGANISM: Medicago sativa

Query Match 30.0%; Score 6; DB 10; Length 966;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 RGGP 14
 Db 11111

Db 642 RGGP 647

RESULT 12
 US-09-968-561A-156
 Sequence 156, Application US/09968561A
 Patent No. US20020164642A1

GENERAL INFORMATION:
 APPLICANT: Tomlinson, Ian M
 APPLICANT: Winter, Gregory M
 TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand

CURRENT APPLICATION NUMBER: US/09/968,561A
 CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: GB 9722131.1

PRIOR FILING DATE: 1997-10-20

PRIOR APPLICATION NUMBER: US 60/065,248

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: PCT/GB98/03135

PRIOR FILING DATE: 1998-10-20

PRIOR APPLICATION NUMBER: US 09/511,939

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 350

SOFTWARE: PatentIn version 3.1

SEQ ID NO 156
 LENGTH: 9

TYPE: PRT
 ORGANISM: Homo sapiens

US-09-968-561A-156

Query Match 25.0%; Score 5; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.8e-04;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 RGGP 13
 Db 3 RGGP 7

RESULT 13
 US-09-192-854-89
 Sequence 89, Application US/09192854
 Patent No. US20020088276A1

GENERAL INFORMATION:
 APPLICANT: Winter, Greg
 APPLICANT: Tomlinson, Ian
 TITLE OF INVENTION: Methods for Selecting Functional Peptides

FILE REFERENCE: 3789/7291

CURRENT APPLICATION NUMBER: US/09/192,854

CURRENT FILING DATE: 1998-11-17

EARLIER APPLICATION NUMBER: 60/066,729

EARLIER FILING DATE: 1997-11-21

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 89
 LENGTH: 9

TYPE: PRT
 ORGANISM: Homo sapiens

US-09-192-854-89

Query Match 25.0%; Score 5; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.8e-04;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 RGGP 13
 Db 3 RGGP 7

RESULT 14
 US-09-826-290-161

US-09-925-301-1634

Db 14 PRGGP 19

Query Match 30.0%; Score 6; DB 10; Length 88;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRGGP 13
 Db 22 PRGGP 27

RESULT 7

US-09-876-889-16

Sequence 16, Application US/09876889

; Patent No. US20020076715A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN

; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSTS

; FILE REFERENCE: 210121-466C3

; CURRENT APPLICATION NUMBER: US/09-876 889

; CURRENT FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 353

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 154

; TYPE: PRT

; ORGANISM: Homo sapien

; US-09-876-889-16

; Query Match 30.0%; Score 6; DB 10; Length 154;

; Best Local Similarity 100.0%; Pred. No. 25;

; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 13 PTSSEQ 18
 Db 64 PTSSEQ 69

; RESULT 8

US-10-067-813-17

; Sequence 17, Application US/10067813

; Patent No. US20020156013A1

; GENERAL INFORMATION:

; APPLICANT: Renaud, Jean-Christophe

; APPLICANT: Louahed, Jamila

; APPLICANT: Grasso, Luigi

; APPLICANT: Levitt, Roy

; APPLICANT: Nicolaides, Nicholas

; TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating

; TITLE OF INVENTION: Atopic Allergies and Related Disorders

; FILE REFERENCE: 036870-5071

; CURRENT APPLICATION NUMBER: US/10/067, 813

; CURRENT FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157, 247

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-18

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 218

; TYPE: PRT

; ORGANISM: R-Ras

; US-10-067-813-17

; Query Match 30.0%; Score 6; DB 9; Length 218;

; Best Local Similarity 100.0%; Pred. No. 33;

; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 8 PRGGP 13
 ; US-10-067-813-17

RESULT 9

US-09-850-048A-2

; Sequence 2, Application US/09850048A

; Patent No. US2002003754A1

; GENERAL INFORMATION:

; APPLICANT: Prockop, Darwin J.

; APPLICANT: Hojima, Yoshiro

; Li, Shi-Wu

; Sieron, Aleksander

; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND

; PROCESSES; METHODS AND USES THEREOF

RESULT 3
US-09-876-204-5
; Sequence 5, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIORITY NUMBER: 09/166,028
; PRIORITY NUMBER: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-876-204-5
Query Match 95.0%; Score 19; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.7e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DGSGEQPRGGGTSSEQIM 20
Db 141 DGSGEQPRGGGTSSEQIM 159

RESULT 4
US-09-876-204-4
; Sequence 4, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIORITY NUMBER: 09/166,028
; PRIORITY NUMBER: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-204-4

Query Match 95.0%; Score 19; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.7e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 GGCGTSSSEQIM 20
Db 10 GGCGTSSSEQIM 20

RESULT 5
US-09-876-204-1
; Sequence 1, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIORITY NUMBER: 09/166,028
; PRIORITY NUMBER: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo sapiens, Mus musculus, and Rattus norvegicus
; NAME/KEY: VARIANT
; LOCATION: (6)..(10)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be O or H;
; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1

Query Match 55.0%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTTSSSEQI 19
Db 11 GGPTTSSSEQI 19

RESULT 6
US-09-925-301-1634
; Sequence 1634, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIORITY NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIORITY NUMBER: 60/124,270
; PRIORITY NUMBER: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1634
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

Query Match 50.0%; Score 10; DB 10; Length 20;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on : January 7, 2003, 12:39:54 ; Search time 7.69231 seconds
 (without alignments)
 49.274 Million cell updates/sec

Title: US-09-876-204-3
 Perfect score: 20
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Scoring table: OLIGO
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Searched: 117078 seqs, 18951520 residues

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Minimum DB seq length: 0
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep;*
6: /cgn2_6/ptodata/1/pubpaa/US07_PTNEW_PUBCOMB.pep;*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep;*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep;*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep;*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep;*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep;*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep;*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep;*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	20	100.0	20	10 US-09-876-204-3
2	19	95.0	331	10 US-09-033-525-2
3	11	55.0	20	10 US-09-876-204-5
4	10	50.0	20	10 US-09-876-204-4
5	9	45.0	19	10 US-09-876-204-1
6	6	30.0	88	10 US-09-925-301-1634
7	7	30.0	154	10 US-09-876-889-16
8	6	30.0	218	9 US-10-067-813-17
9	6	30.0	494	12 US-10-143-002-4
10	6	30.0	730	10 US-09-850-048A-2
11	6	30.0	966	10 US-09-978-698-2
12	5	25.0	9	9 US-09-968-561A-156
13	5	25.0	9	10 US-09-192-854-89
14	5	25.0	14	9 US-09-826-290-161
15	5	25.0	14	9 US-09-826-290-294
16	5	25.0	14	9 US-09-826-290-304
17	5	25.0	14	10 US-09-791-778-92
18	5	25.0	14	10 US-09-791-378-192
19	5	25.0	10	10 US-09-791-378-154

ALIGMENTS

RESULT	Query	Match	Length	DB	ID	Description
1	US-09-876-204-3	20	100.0%	20	10	Length 20;
	Sequence 3, Appli	Best Local Similarity	100.0%	Pred. No.	1.8e13;	DB 10;
	Sequence 2, Appli	Matches 20;	0;	Mismatches	0;	Length 20;
	Sequence 5, Appli	Conservative	0;	Indels	0;	Gaps 0;
	Sequence 4, Appli					
	Sequence 1, Appli					
	Sequence 1634, Appli					
	Sequence 16, Appli					
	Sequence 17, Appli					
	RESULT 2					
	US-09-033-525-2					
	Sequence 2, Application US/09033525					
	Patent No. US2002009033525					
	GENERAL INFORMATION:					
	APPLICANT: Yarkoni, Shai					
	APPLICANT: Ben-Yehudan, Ahmi					
	APPLICANT: Azar, Yehudit					
	APPLICANT: Aqeilan, Rami					
	APPLICANT: Belotsotsky, Ruth					
	APPLICANT: Lorberbaum-Galski, Haya					
	TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING					

					GeCore version 5.1.3
Copyright (c) 1993 - 2003	Compugen Ltd.				
OM protein - protein search, using sw model					
Run on:	January 7, 2003, 12:37:03	:	Search time 13.3333 Seconds		
Title:	US-09-876-204-3		(without alignments)		
Perfect score:	20		144.202 Million cell updates/sec		
Sequence:	1 MDGSGEQPRGGPMSSEQIM 20				
Scoring table:	OLIGO				
Searched:	Gapext 60.0 , Gapext 60.0				
Word size :	283224 seqs, 96134422 residues				
Word size :	0				
Total number of hits satisfying chosen parameters:	283224				
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Post-processing: Listing first 45 summaries					
Database :	PIR_33;*				
1: pir1;*					
2: pir2;*					
3: pir3;*					
4: pir4;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	143	2 I38921	bcl-2-associated protein x, delta splice form - human
2	20	100.0	179	2 JC7255	Bax delta protein
3	20	100.0	192	2 A41538	bcl-2-associated p
4	20	100.0	218	2 B47538	bcl-2-associated p
5	11	55.0	41	2 C47538	bcl-2-associated p
6	10	50.0	192	2 D41538	bcl-2-associated p
7	9	45.0	743	2 T47849	hypothetical prote
8	8	40.0	531	2 T08760	hypothetical prote
9	7	35.0	968	2 T51933	kinesin motor prote
10	7	35.0	1217	2 T00270	hypothetical prote
11	6	30.0	105	2 PWD018	hypothetical prote
12	6	30.0	126	2 T16552	hypothetical prote
13	6	30.0	137	2 G72666	hypothetical prote
14	6	30.0	218	1 TVHURR	transforming prote
15	6	30.0	246	2 B37225	acrosomal protein
16	6	30.0	265	2 A37225	acrosomal protein
17	6	30.0	297	2 S33927	interphotoreceptor
18	6	30.0	298	2 S21965	hypothetical prote
19	6	30.0	302	2 S71334	acetyl xylan ester
20	6	30.0	304	2 A49185	interphotoreceptor
21	6	30.0	311	2 T15957	hypothetical prote
22	6	30.0	337	2 147079	folliculin - shee
23	6	30.0	344	1 A27701	folliculin precu
24	6	30.0	344	2 145894	folliculin - bovi
25	6	30.0	348	2 T25258	hypothetical prote
26	6	30.0	364	2 I45915	interstitial retin
27	6	30.0	370	2 S68415	phosphoenolpyruvat
28	6	30.0	370	2 S68413	phosphoenolpyruvat
29	30.0				
ALIGNMENTS					
RESULT 1					
I38921					
bcl-2-associated protein x, delta splice form - human					
N: Alternative names: BAX; programmed cell death membrane protein x delta					
C: Species: Homo sapiens (man)					
C: Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000					
C: Accession: I38921					
R: Aptie, S.S.; Mattei, M.G.; Olsen, B.R.					
Gentics 26, 592-594, 1995					
Genomics 26, 592-594, 1995					
A: Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a					
A: Reference number: I38921; MUID: 95331797; PMID: 7607685					
A: Accession: I38921					
A: Status: preliminary; nucleic acid sequence not shown; translation not shown					
A: Molecule type: mRNA					
A: Residues: 1-143 <RES>					
A: Cross-references: EMBL:U19599; NID:9841237; PIDN: AAC50142.1; PID:9841238					
C: Genetics:					
A: Gene: GDB:BAX					
A: Cross references: GDB:228082; OMIM:600040					
A: Map position: 19q13.3-19q13.4					
C: Superfamily: bcl transforming protein					
Query Match	100.0%	Score	20;	DB	2;
Best Local Similarity	100.0%	Pred. No.	1e-13;	Length	143;
Matches	20;	Conservative	0;	Mismatches	0;
Db	1	MDGSGEQPRGGPMSSEQIM	20		
RESULT 2					
JC7255					
Bax delta protein - human					
C: Species: Homo sapiens (man)					
C: Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000					
C: Accession: JC7255					
R: Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.					
Biochem. Biophys. Res. Commun. 270, 868-879, 2000					
A: Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.					
A: Reference number: JC7255					
A: Accession: JC7255					
A: Molecule type: mRNA					
A: Residues: 1-179 <SCH>					
A: Cross-references: GB:AF247393					
C: Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It					
C: Superfamily: bcl transforming protein					
Query Match	100.0%	Score	20;	DB	2;
Length	179;				

Best Local Similarity 100.0%; Pred. No. 1.3e-13; Mismatches 0;保守型 0; Indels 0; Gaps 0;

Matches

Qy 1 MDGSGEOPRGGGPSSSEQIM 20
 C;Species: Homo sapiens (man)
 C;Alternate names: BAX; programmed cell death membrane protein x alpha
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C;Accession: A47538
 R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
 Cell, 74, 609-619, 1993
 A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
 A;Reference number: A47538; MUID:93364978; PMID:8358790
 A;Accession: A47538
 A;Molecule type: mRNA
 A;Cross-references: GDB:122473; PIDN:AAA03619.1; PID:9388166
 A;Map position: 19q13.3-19q13.4
 C;Superfamily: bcl transforming protein
 C;Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembrane F;172-191/Domain: transmembrane #status predicted <TMH1>

RESULT 3

Query Match 100.0%; Score 20; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-13; Mismatches 0; Indels 0; Gaps 0;

Matches

Qy 1 MDGSGEOPRGGGPSSSEQIM 20
 Db 1 MDGSGEOPRGGGPSSSEQIM 20

RESULT 4

bcl-2-associated protein x, beta splice form - human
 N;Alternate names: BAX; programmed cell death membrane protein x beta
 C;Species: Homo sapiens (man)
 C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C;Accession: B47538
 R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
 Cell, 74, 609-619, 1993
 A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
 A;Reference number: A47538; MUID:93364978; PMID:8358790
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-192 <OLT>
 A;Cross-references: GB:L22472
 C;Genetics:
 A;Gene: bax
 A;Superfamily: bcl transforming protein

RESULT 5

bcl-2-associated protein x, gamma splice form - human
 N;Alternate names: BAX; programmed cell death membrane protein x gamma
 C;Species: Homo sapiens (man)
 C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
 C;Accession: C47538
 R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
 Cell, 74, 609-619, 1993
 A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
 A;Reference number: A47538; MUID:93364978; PMID:8358790
 A;Molecule type: mRNA
 A;Residues: 1-41 <OLT>
 A;Cross-references: GB:L22475; PIDN:9388169; PIDN:AAA03621.1; PID:9388170
 A;Note: the amino end of the mature protein is blocked

Matches

Qy 1 MDGSGEOPRGG 11.
 Db 1 MDGSGEOPRGG 11

RESULT 6

bcl-2-associated protein x - mouse
 N;Alternate names: BAX; programmed cell death membrane protein x
 C;Species: Mus musculus (house mouse)
 C;Accession: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
 C;Accession: D47538
 R;Oltvai, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
 Cell, 74, 609-619, 1993
 A;Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates apoptosis
 A;Reference number: A47538; MUID:93364978; PMID:8358790
 A;Accession: D47538
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-192 <OLT>
 A;Cross-references: GB:L22472
 C;Genetics:
 A;Gene: bax
 A;Superfamily: bcl transforming protein

RESULT 7

hypothetical protein T8810.40 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: T47849
 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lencke, K.; Maye submitted to the Protein Sequence Database, March 2000
 A;Reference number: Z24478
 A;Accession: T47849
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-743 <RIE>

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 192;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

Qy 1 MDGSGEQPRGGPSSSEQIM 20
 Db 1 MDGSGEQPRGGPSSSEQIM 20

A;Cross-references: EMBL:AL138846
A;Experimental source: cultivar Columbia: BAC clone T8B10
C;Genetics:
A;Map position: 3
A;Note: T8B10.40

Query Match 45.0%; Score 9; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 SEQOPRG 12
Db 725 SEQOPRG 733

RESULT 8
T08760
hypothetical protein DKFZP586M1019.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08760
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08760
A;Molecule type: mRNA
A;Residues: 1-531 <WAM>
A;Cross-references: EMBL:AL050284
A;Experimental source: adult uterus; clone DKFZP586M1019
C;Genetics:
A;Note: DKFZP586M1019.1

Query Match 40.0%; Score 8; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.86; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GEGOPRG 12
Db 117 GEGOPRG 124

RESULT 9
T51933
kinesin motor protein [imported] - smut fungus (*Ustilago maydis*)
C;Species: *Ustilago maydis* (corn smut)
C;Date: 20-oct-2000 #sequence_revision 20-oct-2000 #text_change 31-Dec-2000
C;Accession: T51933
R;Lehmler, C.; Steinberg, G.; snetselaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.
ENBO J. 16, 3464-3473, 1997
A;Title: Identification of a motor protein required for filamentous growth in *Ustilago maydis*
A;Reference number: 220770; PMID:9218789
A;Accession: T51933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-968 <LEH>
A;Cross-references: EMBL:U92845; PIDN:AAB63337.1
C;Genetics:
A;Gene: kin2
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
Query Match 35.0%; Score 7; DB 2; Length 968;
Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 RGGGPGTS 15
Db 921 RGGGPGTS 927

RESULT 10
T00270
hypothetical protein KIAA0596 - human (fragment)
C;Species: Homo sapiens (man)

RESULT 11
PW0018
hypothetical protein 105 - *Micromonospora* sp. (fragment)
C;Species: *Micromonospora* sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C;Accession: PW0018
R;Kelemen, G.H.; Cundliffe, E.; Finansek, I.
Gene 98 53-60, 1991
A;Title: Cloning and characterization of gentamicin-resistance genes from *Micromonospora*
A;Reference number: JG0017; MUID:9192615; PMID:2013410
A;Accession: PW0018
A;Molecule type: DNA
A;Residues: 1-105 <KEL>
A;Cross-references: GB:MS5521
A;Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a

Query Match 30.0%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 23; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 GGPTSS 16
Db 81 GGPTSS 86

RESULT 12
T16952
hypothetical protein T28D9.10 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16952
R;Fulton, L.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of *C. elegans* cosmid T28D9.
A;Reference number: Z18614
A;Accession: T16952
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-26 <FUL>
A;Cross-references: EMBL:U28738; NID:9861262; PID:9861268; PIDN:AAA68313.1; CESP:T28D
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T28D9.10
A;Introns: 27/1; 62/1; 96/1

Query Match 30.0%; Score 6; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 28; Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 Qy 8 PRGGP 13
 |||||
 Db 119 PRGGP 124

RESULT 14
 TVHURR
 transforming protein R-ras - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-Jan-2001
 C;Accession: A26159
 R;Lowe, D.G.; Capon, D.J.; Delwart, E.; Sakaguchi, A.Y.; Naylor, S.L.; Goeddel, D.V.
 Cell 48, 137-146, 1987
 A;Title: Structure of the human and murine R-ras genes, novel genes closely related to r
 A;Reference number: A26159; MUID:87078390; PMID:3098437
 A;Accession: A26159
 A;Molecule type: DNA
 C;Genetics:
 A;Gene: APE0758
 A;Molecule type: mRNA
 A;Residues: 1-137 <WIL>
 A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79735.1; PID:951043521; PID:951043521
 A;Experimental source: strain K1
 C;Superfamily: Aeropyrum pernix hypothetical protein APE0758
 Query Match 30.0%; Score 6; DB 2; Length 137;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 OPRGG 12
 |||||
 Db 85 QPRGGG 90

RESULT 14
 TVHURR
 transforming protein R-ras - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-Jan-2001
 C;Accession: A26159
 R;Lowe, D.G.; Capon, D.J.; Delwart, E.; Sakaguchi, A.Y.; Naylor, S.L.; Goeddel, D.V.
 Cell 48, 137-146, 1987
 A;Title: Structure of the human and murine R-ras genes, novel genes closely related to r
 A;Reference number: A26159; MUID:87078390; PMID:3098437
 A;Accession: A26159
 A;Molecule type: DNA
 A;Residues: 1-218 <LOW>
 A;Cross-references: GB:MI4949; NID:9190934; PIDN:AAA60256.1; PID:9190936
 A;Gene: GDB:RRAS
 A;Map position: 19q13.3-19qter
 A;Cross-references: GDB:120356; OMIM:165090
 A;Introns: 51/3; 81/1; 115/2; 151/3; 191/2
 C;Superfamily: ras transforming protein; translation elongation factor Tu homology
 C;Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleot
 F;30-145/Domain: translation elongation factor Tu homology <ERU>
 F;36-42/Region: nucleotide-binding motif A (P-loop)
 F;142-145/Region: GTP-binding NRK1 motif
 F;172-174/Region: GTP-binding SAK/L motif
 F;42-43,6,1142-143,145-172/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta
 F;215/Modified site: geranyl-geranyl (Cys) (covalent) #status predicted
 F;215/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 30.0%; Score 6; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 PRGGP 13
 |||||
 Db 14 PRGGP 19

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OM protein -> protein search, using sw model

Run on: January 7, 2003, 12:27:38 ; Search time 25.1282 Seconds
(without alignments)
163.997 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106

Sequence: 1 MDGSGEQPRGGPSSSEQIM 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL 21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	106	100.0	24	4 Q8WXL1	Q8WXL1 PRELIMINARY; PRT: 24 AA.
2	106	100.0	164	4 Q9UD06	Q9UD06; 01-MAR-2002 (TREMBrel 20', Created)
3	106	100.0	179	4 Q9NNG7	01-MAR-2002 (TREMBrel 20, Last sequence update)
4	97	91.5	192	6 Q85043	01-MAR-2002 (TREMBrel 20, Last annotation update)
5	83	78.3	24	11 Q8PHY7	BC12-associated X protein (Fragment).
6	54	50.9	302	3 Q99034	BAX.
7	52	49.1	402	4 Q9NS06	Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo sapiens (Human); Catarrhini; Hominidae; Homo.
8	52	49.1	403	4 Q9C009	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
9	52	49.1	475	16 Q9ZRZ5	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
10	51	48.1	658	5 Q9NR86	RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
11	50	47.2	213	0 Q9SBR7	RL DR FT NON_TER 24 AA: 2379 MW: 8C3D3EB8B7479B798 CRC64;
12	50	47.2	495	12 Q918P0	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
13	50	47.2	743	10 Q9M221	RT DR FT NON_TER 24 AA: 2379 MW: 8C3D3EB8B7479B798 CRC64;
14	49.5	46.7	743	4 Q96AV4	Best local Similarity 100.0%; Score 106; DB 4; Length 24; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15	49.5	46.7	715	4 Q96J14	QY 1 MDGSGEQPRGGPSSSEQIM 20 PRELIMINARY; PRT: 164 AA.
16	46.7	778	4 Q8TDC2	Db 1 MDGSGEQPRGGPSSSEQIM 20 DT DT 01-MAY-2000 (TREMBrel 13, Created) DT 01-MAY-2000 (TREMBrel 13, Last sequence update) DT 01-JUN-2002 (TREMBrel 21, Last annotation update)	

ALIGNMENTS

RESULT	ID	SEQUENCE	DESCRIPTION
1	Q8WXL1	Q8WXL1	Q8WXL1 PRELIMINARY; PRT: 24 AA.
2	Q9UD06	Q9UD06	Q9UD06; 01-MAR-2002 (TREMBrel 20', Created)
3	Q9NNG7	Q9NNG7	01-MAR-2002 (TREMBrel 20, Last sequence update)
4	Q85043	Q85043	01-MAR-2002 (TREMBrel 20, Last annotation update)
5	Q8PHY7	Q8PHY7	BC12-associated X protein (Fragment).
6	Q99034	Q99034	BAX.
7	Q9NS06	Q9NS06	Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo sapiens (Human); Catarrhini; Hominidae; Homo.
8	Q9C009	Q9C009	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
9	Q9ZRZ5	Q9ZRZ5	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
10	Q9NR86	Q9NR86	RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
11	Q9SBR7	Q9SBR7	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
12	Q918P0	Q918P0	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
13	Q9M221	Q9M221	SEQUENCE FROM N.A. Thornborow E.C., Schwartzbarb E.M., Manfredi J.J.; RT A conserved intronic response element mediates direct p53-dependent transcriptional activation of both the human and murine bax genes.";
14	Q96AV4	Q96AV4	Best local Similarity 100.0%; Score 106; DB 4; Length 24; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15	Q96J14	Q96J14	QY 1 MDGSGEQPRGGPSSSEQIM 20 PRELIMINARY; PRT: 164 AA.
16	Q8TDC2	Q8TDC2	Db 1 MDGSGEQPRGGPSSSEQIM 20 DT DT 01-MAY-2000 (TREMBrel 13, Created) DT 01-MAY-2000 (TREMBrel 13, Last sequence update) DT 01-JUN-2002 (TREMBrel 21, Last annotation update)

DE Bax epsilon.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99120940; Pubmed=990818;
 RA Shi B., Tribe D., Kajiji S., Iwata K.K., Bruskin A., Mahajna J.;
 RT "Identification and characterization of baxepsilon, a novel bax
 variant missing the BH2 and the transmembrane domains.";
 RL Biochem Biophys Res Commun. 254:779-785(1999).
 DR EMBL: AF007826; ARD22705; 1; -.
 DR InterPro: IPR000712; BCL2_BH.
 DR InterPro: IPR002455; BCL2_family.
 DR Pfam: PF00452; BCL1-2; 1.
 DR SMART: SM00332; BCL1; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR SEQUENCE 164 AA; 18129 MW; 12CCDBB073ER4C9E CRC64;

Query Match 100.0%; Score 106; DB 4; Length 164;
 Best Local Similarity 100.0%; Pred. No. 5.9e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPREGGPPSSEQIM 20
 Db 1 MDGSGEQPREGGPPSSEQIM 20

RESULT 3
 ID 09NYG7 PRELIMINARY; PRT; 179 AA.
 AC 09NYG7;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Bax-sigma.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=202307095; Pubmed=1072918;
 RA Schmitt B., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;
 RT "Characterization of bax-sigma, a cell death-inducing isoform of
 Bax.";
 RL Biochem Biophys Res Commun. 270:868-879(2000).
 DR EMBL: AF247393; AF21267; 1; -.
 DR InterPro: IPR00712; BCL2_BH.
 DR Pfam: PF00452; BCL2_family.
 DR SMART: SM00337; BCL1; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2B4CE CRC64;

Query Match 100.0%; Score 106; DB 4; Length 179;
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPREGGPPSSEQIM 20
 Db 1 MDGSGEQPREGGPPSSEQIM 20

RESULT 4
 ID 08S043 PRELIMINARY; PRT; 192 AA.
 AC 08S043;
 ID 099034 PRELIMINARY; PRT; 302 AA.
 AC 099034;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE ACETYLXYLAN esterase precursor (EC 3.1.1.72).
 AXEL.
 OS Trichoderma reesei (Hypocreales; Hypocreaceae; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocreales).

RESULT 5
 ID 08VH7 PRELIMINARY; PRT; 24 AA.
 AC 08VH7;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)
 DE Bcl2-associated X protein (Fragment).
 GN BAX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurobathy; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Thorntorow E.C., Schwartzbarf E.M., Manfredi J.J.;
 RT "A conserved intronic response element mediates direct p53-dependent
 transcriptional activation of both the human and murine bax genes.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF339055; AAL7334.1; -.
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

Query Match 78.3%; Score 83; DB 11; Length 24;
 Best Local Similarity 85.0%; Pred. No. 2.9e-06;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDGSGEQPREGGPPSSEQIM 20
 Db 1 MDGSGEQPREGGPPSSEQIM 20

RESULT 6
 ID 099034 PRELIMINARY; PRT; 302 AA.
 AC 099034;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE ACETYLXYLAN esterase precursor (EC 3.1.1.72).
 AXEL.
 OS Trichoderma reesei (Hypocreales; Hypocreaceae; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocreales).

RESULT 7
 ID 099035 PRELIMINARY; PRT; 24 AA.
 AC 099035;
 ID 099036 PRELIMINARY; PRT; 24 AA.
 AC 099036;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE ACETYLXYLAN esterase precursor (EC 3.1.1.72).
 AXEL.
 OS Trichoderma reesei (Hypocreales; Hypocreaceae; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocreales).

OK NCBI_TAXID=51453;

RN [1] RESULT 7

RP SEQUENCE FROM N A., SEQUENCE OF 158-186, AND CHARACTERIZATION.

RC ID Q9NS06 PRELIMINARY; PRT; 402 AA.

RK ID Q9NS06; PRELIMINARY; PRT; 402 AA.

RA AC Q9NS06; PRELIMINARY; PRT; 402 AA.

RT DT 01-OCT-2000 (TREMBLrel. 15, Created)

RA Margoilles-Clark E.; Tenkanen M.; Soederlund H.; Penttilae M.;

RT Eur. J. Biochem. 237:553-560(1996).

RL DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

RL DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

RN DE Winged helix/forkhead transcription factor.

RN HFH1.

RP FUNCTION.

RC STRAT="RUTC-30;

RA Poutanen K.; Sundberg M.; Korte H.; Puls J.;

RT "Deacetylation of xylans by acetyl esterases of Trichoderma reesei.";

RL Appl. Microbiol. Biotechnol. 33:506-510(1990).

RN [3] RN

RP CHARACTERIZATION.

RC STRAT="RUTC-30;

RA Sundberg M.; Poutanen K.;

RT "Purification and properties of two acetylxytan esterases of Trichoderma reesei";

RL Biotechnol. Appl. Biochem. 13:1-11(1991).

RN [4]

X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RX MEDLINE=98137545; PubMed=9761918;

RA Hakulinen N.; Tenkanen M.; Rouvinen J.;

RT "Crystallization and preliminary X-ray diffraction studies of the catalytic core of acetyl xytan esterase from Trichoderma reesei.";

RL Acta Crystallogr D 54:430-432(1998).

CC [-] FUNCTION: DEGRADATION ACETYLATED XYLAN BY CLEAVING ACETYL SIDE GROUPS FROM THE HETERO-XYLAN BACKBONE.

CC [-] CATALYTIC ACTIVITY: DEACETYLATION OF XYLANS AND XYLO-OLIGOSACCHARIDES.

CC [-] ENZYME REGULATION: INHIBITED BY PHENYL METHYL SULFONYL FLUORIDE.

CC [-] PATHWAY: XYLAN DEGRADATION.

CC [-] SUBCELLULAR LOCATION: EXTRACELLULAR.

CC [-] PTM: GLYCOSTYLATED.

CC [-] MASS SPECTROMETRY: MW=21805; METHOD=MALDI.

DR EMBL; CAR3247.1; -.

DR HSSP; F00725; ZCBH.

DR InterPro; IPR000254; CBD_fungal.

DR InterPro; IPR000675; Cutinase.

DR InterPro; IPR000734; Lipase.

DR Pfam; PF00734; CEM_1..1.

DR ProDom; PD001821; CBD_fungal; 1.

DR SMART; SM00236; fcBD; 1.

PROSITE; PS00562; CBD_FUNGAL; FALSE_NEG.

DR PROSTB; PS00120; LIPASE_SER; UNKNOWN1.

KW cellulose degradation; Hydrolase; Serine esterase; Glycoprotein;

KW 3D-structure; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT PROPEP 21 31 ACETYLXYLAN ESTERASE.

FT CHAIN 32 302 LINKER (BY SIMILARITY).

FT DOMAIN 244 266 CELLULOSE-BINDING (BY SIMILARITY).

FT DOMAIN 267 302 BLOCKED.

FT MOD_RES 32 32 ACT_SITE 121 121 BY SIMILARITY.

FT DISULFID 274 291 BY SIMILARITY.

FT CARBOHYD 285 301 BY SIMILARITY.

FT CARBOHYD 94 94 N-LINKED (GLCNAC, .) (PROBABLE).

SQ SEQUENCE 302 AA; 30754 MW; BB6EDCA2971A9F2A CR64;

Query Match Best local Similarity 49.1%; Score 52; DB 4; Length 402; Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Q9NS06 3 GSSEQPREGGGPSPSEQI 19 | ||| | ||| : | |

Db 61 GDGEOSAGGGPGEAAI 77

RESULT 8

Q9C009 ID Q9C009 PRELIMINARY; PRT; 403 AA.

AC Q9C009; PRELIMINARY; PRT; 403 AA.

DT DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)

RA DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE HNF-3/forkhead-like protein 1.

GN HNF1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.

RN NCBI_TAXID=9606;

[1] RN

RP SEQUENCE FROM N A.

RA Bieleler A.; Pasche B.; Frank S.; Kunz J.; Zoll B.;

RT "isolation and characterization the human fork head gene HFH-1..";

RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF22550; RAK00639.1; -.

DR HSSP; 063245; 2HIF.

DR InterPro; IPR001766; TF_Fork_head.

DR Pfam; PF00250; Fork_head.

DR PRINTS; PR00053; FORKHEAD.

DR SMART; SM00339; FH; 1.

DR PROSITE; PS00658; FORK_HEAD_2; 1.

DR PROSITE; PS00039; FORK_HEAD_3; 1.

SQ SEQUENCE 403 AA; 41491 MW; EH52255AEAC6929B CRC64;

Best Local Similarity 50.0%; Score 54; DB 3; Length 302;

Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Q9NS06 1 MGCGSGOPRGPGPTTSQ 18 | ||| | ||| ;

Db 237 LSGGsQPPGGGPTTSR 254

b	62	DGGBQSAGGGPAGBEAI	78
RESULT 9			
92RZ5	PRELIMINARY;	PRT;	475 AA.
D 092RZ5;			
092RZ5;			
T 01-DEC-2001 (TREMBLrel. 19, Created)			
T 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
E 01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
E Chemotaxis protein (Motility protein D).			
MOTD OR R00676 OR SMC03044.			
Rhizobium meliloti (Sinorhizobium meliloti).			
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
Rhizobiaceae; Sinorhizobium.			
NCBI_TaxID=382;			
[1]			
SEQUENCE FROM N.A.			
STRAIN=1021;			
X MEDLINE=21396507; PubMed=11818430;			
X Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,			
X Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,			
X Godt T., Goiffon A., Kahn D., Kiss V., Lelauze V., Masuy D.,			
X Pohl T., Portebeau D., Puebler A., Purnelle B., Ramsperger U.,			
X Reward C., Thebaud P., Vandembrouck M., Weidner S., Galibert F.;			
X "Analysis of the chromosome sequence of the legume symbiont			
X Sinorhizobium meliloti strain 1021.";			
X PROC. NATL. ACAD. SCI. U.S.A. 98:9877-9882(2001).			
X EMBL; AU591784; CAD45248.1; -.			
W Complete proteome.			
SEQUENCE 475 AA;	49124 MW;	8177547429DD4425 CRC64;	
Query Match 49.1%; Score 52; DB 16; Length 475;			
Best Local Similarity 52.9%; Pred. No. 5.9;			
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;			
Y 2 DGSEQPRGGPSSSEQ 18			
b 435 DGQGRQPRDGGRRAATER 451			
RESULT 10			
9NBR6	PRELIMINARY;	PRT;	658 AA.
C 09NBR6;			
C 01-OCT-2000 (TREMBLrel. 15, Created)			
T 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
T 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
P Possible putative cell division related protein.			
N CHRL177.			
S Trypanosoma brucei.			
S Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.			
X NCBI_TaxID=5691;			
[1]			
N SEQUENCE FROM N.A.			
C STRAIN="TREU927";			
A Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,			
A Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,			
A Gerrard C., Rajandream M.A., Barrell B.G.;			
L Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
L -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
C -!- SIMILARITY: CONTAINS 1 NYB-LIKE DOMAIN.			
EMBL; AL359782; CAB95467.1; -.			
HSSP; P25685; IHDU.			
InterPro; IPR001623; DnaJ_N.			
InterPro; IPR003095; Hsp_DnaJ.			
InterPro; IPR001005; MyDNA_binding.			
RESULT 11			
Q9SBR7	PRELIMINARY;	PRT;	213 AA.
ID Q9SBR7;			
AC Q9SBR7;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE EndoGCRP5 protein.			
DR ENDOGRP5.			
OS Medicago varia.			
EC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spematophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicagogo			
OX NCBI_TaxID=36902;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=ROOT NODULES;			
RA MEDLINE=20120383; PubMed=105656590;			
RT Jimenez-Zurdo J.I., Frigier F., Crespi M.D., Kondorosi A.;			
RT "Expression profiles of 22 novel molecular markers for organogenetic			
RT pathways acting in alfalfa nodule development.,";			
RL Mol. Plant Microbe Interact. 13:96-106(2000).			
DR EMBL; AJ248329; CAB65282.1; -.			
SQ SEQUENCE 213 AA;	231429 MW;	137C629ED1D9872A CRC64;	
Query Match 47.2%; Score 50; DB 10; Length 213;			
Best Local Similarity 52.9%; Pred. No. 5;			
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;			
QY 3 GSGCQPRGGPSSSEQI 19			
Db 90 GSGBENNGGEEEGEOV 106			
RESULT 12			
Q918P0	PRELIMINARY;	PRT;	495 AA.
ID Q918P0;			
AC Q918P0;			
DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Latency associated antigen.			
GN ORF3.			
OS Ovine herpesvirus 2.			
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC Gammaparvovirinae.			
OX NCBI_TaxID=10398;			
[1]			
RN SEQUENCE FROM N.A.			
RP Collier L.J., Reid H.W.;			
RT "Isolation and expression of three open reading frames (ORFs) from			
RT ovine herpesvirus 2.,";			
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AR410847; AR05844.1; -.			
SQ SEQUENCE 495 AA;	495166 MW;	2D3B7651085693F CRC64;	

Query Match 47.2%; Score 50; DB 12; Length 495;
 Best Local Similarity 56.2%; Pred. No. 13; Mismatches 1; Indels 6; Gaps 0;

Qy 3 GSQEOPRGGGTTSSEQ 18
 Db 255 GEGEGPGGGPGE 270

RESULT 13
 Q9M221 PRELIMINARY; PRT: 743 AA.
 AC Q9M221;
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 82.6 kDa protein.
 GN TBL0_40.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1] SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AL138646; CAB81824; I;
 DR InterPro: IPR000977; DNA_ligase.
 DR PROSITE: PS00697; DNA_LIGASE_A1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 743 AA; 82639 MW; EB30CA4906AC05E2 CRC64;

Query Match 47.2%; Score 50; DB 10; Length 743;
 Best Local Similarity 100.0%; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SGEQOPRGG 12
 Db 725 SGEPQRGG 733

RESULT 14
 Q96AV4 PRELIMINARY; PRT: 473 AA.
 AC Q96AV4;
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 50.8 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RP SEQUENCE FROM N.A.
 RX MEDLINE:21245130; Pubmed=11347906;
 RA Nagase T., Nakajima M., Nakajima D., Kikuno R., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro.";
 RL DNA Res. 8:85-95(2001).
 DR EMBL: AB058714; BAB4740.1; -.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Serin_tyr_Pkinase.
 DR InterPro: IPR000449; UBA_domain.
 DR Pfam: PF00169; Pkinase_1.
 DR ProDom: PD00001; Euk_Pkinase; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 FT NON-TER 1 1
 SQ SEQUENCE 715 AA; 78499 MW; B90F6EE115C418A5 CRC64;

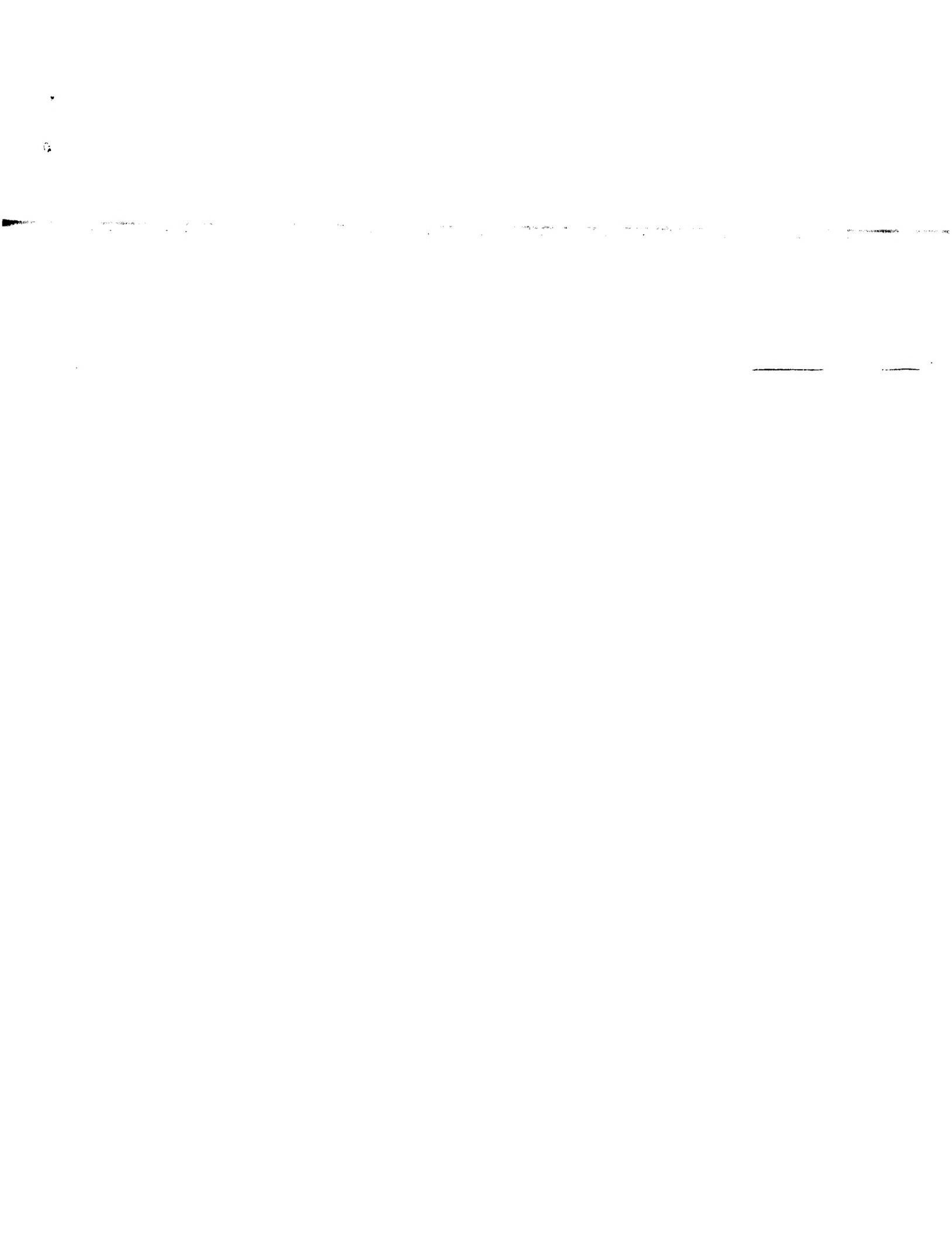
Query Match 46.7%; Score 49.5%; DB 4; Length 715;
 Best Local Similarity 52.6%; Pred. No. 23; Mismatches 4; Indels 1; Gaps 1;

Qy 3 GSQEOPRGG-TTSSEQ 20
 Db 397 GAGDEARGGSPTSKOTL 415

Search completed: January 7, 2003, 12:30:49
 Job time : 27.1282 secs

SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: BC016681; AAH16681; -.
 DR InterPro: IPR000449; UBA_domain.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 50750 MW; D27DAD437DA98AA9 CRC64;

Query Match 46.7%; Score 49.5%; DB 4; Length 473;
 Best Local Similarity 52.6%; Pred. No. 15; Mismatches 4; Indels 1; Gaps 1;



Run on: January 7, 2003, 12:29:33 ; Search time 140 Seconds
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GenCore version 5.1.3

Score No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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Sequence 3, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 3, Appli

RESULT 2
PCT-US99-24747-1
Sequence 1, Application PC/TUS9924747
GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachael M.
TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT-US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-1

Query Match 100.0%; Score 106; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Length: 70

Qy 1 MDGSGEQPRGGPPSSEQIM 20
Db 1 MDGSGEQPRGGPPSSEQIM 20

RESULT 3
PCT-US99-24747-5
Sequence 5, Application PC/TUS9924747
GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachael M.
TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT-US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 5
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-5

Query Match 100.0%; Score 106; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Length: 70

Qy 1 MDGSGEQPRGGPPSSEQIM 20
Db 1 MDGSGEQPRGGPPSSEQIM 20

RESULT 4
PCT-US99-24747-3
Sequence 3, Application PC/TUS9924747
GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachael M.
TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT-US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match 100.0%; Score 106; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.2e-06; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Length: 78

Qy 1 MDGSGEQPRGGPPSSEQIM 20
Db 1 MDGSGEQPRGGPPSSEQIM 20

RESULT 7
PCT-US99-24747-7
Sequence 7, Application PC/TUS9924747
GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachael M.
TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
FILE REFERENCE: 6029-1754
CURRENT APPLICATION NUMBER: PCT-US99/24747
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 34

Query Match 100.0%; Score 106; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Length: 70

Qy 1 MDGSGEQPRGGPPSSEQIM 20
Db 1 MDGSGEQPRGGPPSSEQIM 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US99-24747-7

RESULT 8
Query Match 100.0%; Score 106; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1, 2e-06;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachel M.

TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides

FILE REFERENCE: 6029-5756

CURRENT APPLICATION NUMBER: US/09/177,315

CURRENT FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3
LENGTH: 78
TYPE: PRT

ORGANISM: Homo sapiens
US-09-177-315-3

Query Match 100.0%; Score 106; DB 15; Length 78;
Best Local Similarity 100.0%; Pred. No. 1, 2e-06;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Johnson Jr., Eugene M.
APPLICANT: Easton, Rachel M.

TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides

FILE REFERENCE: 6029-5756

CURRENT APPLICATION NUMBER: US/09/177,315

CURRENT FILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 131
TYPE: PRT

ORGANISM: Human
PCT-US99-05359-2

Query Match 100.0%; Score 106; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2, 1e-06;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Roth, Jack A.

APPLICANT: SWISHER, STEVEN G.

APPLICANT: McDONNELL, TIMOTHY J.

APPLICANT: FANG, BINGLIANG

APPLICANT: BRUCKHEIMER, ELIZABETH

APPLICANT: SARKISS, MONA

APPLICANT: JI, LIN

APPLICANT: ROTH, JACK A.

TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY ADENOVIRAL MEDIATED GENE DELIVERY

FILE REFERENCE: INGN:0088/INCN:008P

CURRENT APPLICATION NUMBER: US/09/266,465

CURRENT FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: 60/077,541

EARLIER FILING DATE: 1998-03-11

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 131
TYPE: PRT

ORGANISM: Human
US-09-266-465-2

Query Match 100.0%; Score 106; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 2, 1e-06;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Pylyos, Inc.

TITLE OF INVENTION: Polypeptides Interactive with BCL-XL

RESULT 12
PCT-US02-06951-242
Sequence 242; Application PC/TUS200206951

GENERAL INFORMATION:
APPLICANT: Pylyos, Inc.

TITLE OF INVENTION: Polypeptides Interactive with BCL-XL

RESULT 10
PCT-US99-05359-2
Sequence 2; Application PC/TUS9905359

FILE REFERENCE: 50036/050W02
 CURRENT APPLICATION NUMBER: PCT/US02/06951
 PRIOR APPLICATION NUMBER: US 60/274,526
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 253
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 242
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 13
 US-10-092-750-242
 Sequence 242; Application US/10092750
 GENERAL INFORMATION:
 APPLICANT: Hammond, Philip W.
 APPLICANT: Alpin, Julia
 APPLICANT: Wright, Martin C.
 TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
 FILE REFERENCE: 50036/050002
 CURRENT APPLICATION NUMBER: US/10/092,750
 CURRENT FILING DATE: 2002-03-07
 PRIOR APPLICATION NUMBER: US 60/274,526
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 253
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 242
 LENGTH: 135
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 14
 US-09-791-537-52874
 Sequence 52874; Application US/09791537
 GENERAL INFORMATION:
 APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Dancer, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 52874
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 15
 US-60-350-061-261
 Sequence 261; Application US/60350061
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH SRC TYROSINE KINASES AND THE SRC TYROSINE KINAS
 FILE REFERENCE: D0185
 CURRENT APPLICATION NUMBER: US/60/350,061
 CURRENT FILING DATE: 2002-01-18
 NUMBER OF SEQ ID NOS: 981
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 261
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 16
 US-60-350-061-261
 Sequence 261; Application US/60350061
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH SRC TYROSINE KINASES AND THE SRC TYROSINE KINAS
 FILE REFERENCE: D0185
 CURRENT APPLICATION NUMBER: US/60/350,061
 CURRENT FILING DATE: 2002-01-18
 NUMBER OF SEQ ID NOS: 981
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 261
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 106; DB 24; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2.2e-06; Mismatches 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSEQPRGGPSSSEQIM 20
 1 MDGSEQPRGGPSSSEQIM 20

Db 1 MDGSEQPRGGPSSSEQIM 20

Search completed: January 7, 2003, 12:36:30
 Job time : 141 secs

Query Match 100.0%; Score 106; DB 27; Length 143;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06; Mismatches 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSEQPRGGPSSSEQIM 20
 1 MDGSEQPRGGPSSSEQIM 20

Db 1 MDGSEQPRGGPSSSEQIM 20

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 7, 2003, 12:29:58 : Search time 11.7949 Seconds
 (without alignments)
 120.181 Million cell updates/sec

Title: US-09-876-204-3
 Perfect score: 106
 Sequence: 1 MDGSGEQPRGGPSSSEQIM 20

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum Match length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending Patents AA New:*

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3: /cgn2_6/pctodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/pctodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/pctodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/pctodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/pctodata/2/paa/US60_NEW_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	192	1 PCT-US02-38191-5	Sequence 5, Appli
2	106	100.0	192	6 US-10-306-878-5	Sequence 5, Appli
3	101	95.3	191	6 US-10-196-793-46	Sequence 46, Appli
4	52	49.1	402	1 PCT-US02-06001-32	Sequence 32, Appli
5	52	49.1	402	6 US-10-274-177-18	Sequence 18, Appli
6	52	49.1	402	6 US-10-087-080-32	Sequence 32, Appli
7	44.3	73	1 PCT-US02-32727-25717	Sequence 25717, A	
8	47	44.3	73	1 PCT-US02-32727-29374	Sequence 29374, A
9	47	44.3	73	6 US-10-051-498-25717	Sequence 25717, A
10	47	44.3	220	5 US-09-724-676-55403	Sequence 55403, A
11	47	44.3	220	5 US-09-724-676-55403	Sequence 55403, A
12	45	42.5	94	1 PCT-US02-32727-10714	Sequence 10714, A
13	45	42.5	94	6 US-10-276-774-1847	Sequence 10714, A
14	44	41.5	131	6 US-10-276-774-1847	Sequence 1847, AP
15	44	41.5	256	5 US-09-724-676-64338	Sequence 64338, A
16	44	41.5	256	5 US-09-724-676-64341	Sequence 64341, A
17	44	41.5	256	5 US-09-724-676-64345	Sequence 64345, A
18	44	41.5	256	5 US-09-724-676-64345	Sequence 64346, A
19	44	41.5	256	5 US-09-724-676-64348	Sequence 64348, A
20	44	41.5	256	5 US-09-724-676-64341	Sequence 64341, A
21	44	41.5	256	5 US-09-724-676-64345	Sequence 64345, A
22	44	41.5	256	5 US-09-724-676-64346	Sequence 64346, A
23	43	40.6	352	5 US-09-724-676-50097	Sequence 50097, A
24	43	40.6	352	5 US-09-724-676-50098	Sequence 50098, A
25	43	40.6	352	5 US-09-724-676-50097	Sequence 50097, A
26	43	40.6	352	5 US-09-724-676A-50098	Sequence 50098, A

ALIGNMENTS

```

RESULT 1
PCT-US02-38191-5
; Sequence 5, Application PC/TUS0238191
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
TITLE OF INVENTION: Methods for Identifying Modulators of
FILE REFERENCE: FP-IJ 5483
CURRENT APPLICATION NUMBER: PCT/US02/38191
CURRENT FILING DATE: 2002-11-27
PRIORITY APPLICATION NUMBER: US 60/334,149
PRIORITY FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-38191-5
Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSGEQPRGGPSSSEQIM 20
Db 1 MDGSGEQPRGGPSSSEQIM 20

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RESULT 2

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US-10-306-878-5
; Sequence 5, Application US/10306878
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
TITLE OF INVENTION: Methods for Identifying Modulators of
FILE REFERENCE: P-LJ 555
CURRENT APPLICATION NUMBER: US/10/306,878
CURRENT FILING DATE: 2002-11-27
PRIORITY APPLICATION NUMBER: US 60/334,149
PRIORITY FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
; LENGTH: 192
; TYPE: PRT

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; ORGANISM: Homo sapiens
; US-10-306-878-5

Query Match 100.0%; Score 106; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSGEQPRGGPPTSSEQIM 20
Db 1 MDGSGEQPRGGPPTSSEQIM 20

RESULT 3
US-10-196-793A-46
; Sequence 46, Application US/10196793A
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MARTIN G.
; APPLICANT: LIU, YUYING
; TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS
; FILE REFERENCE: CLFR-01US
; CURRENT APPLICATION NUMBER: US/10/196,793A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 60/360,361
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/332,886
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 46
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-196-793A-46

Query Match 95.3%; Score 101; DB 6; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DGSEBOPRGGPSSSEQIM 20
Db 1 DGSOPRGGPSSSEQIM 19

RESULT 4
PCT-US02-0601-32
; Sequence 32, Application PC//US0206001
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840PC
; CURRENT APPLICATION NUMBER: PCT//US02/06001
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: winged helix/forkhead transcription factor (HFL1)

RESULT 5
US-10-274-177-18
; Sequence 18, Application US/10274177
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/274,177
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/229,345
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-274-177-18

Query Match 49.1%; Score 52; DB 1; Length 402;
Best Local Similarity 58.8%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GSGOPRGGPPTSSEQI 19
Db 61 GDGBOSAGGGPAGAEAI 77

RESULT 6
US-10-087-080-32
; Sequence 32, Application US/10087080
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: Novel Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: winged helix/forkhead transcription factor (HFL1)

Query Match 49.1%; Score 52; DB 6; Length 402;
Best Local Similarity 58.8%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 4 GSGOPRGGPPTSSEQI 19
Db 61 GDGBOSAGGGPAGAEAI 77

QY 3 GSSEQPRGGPPSSEQI 19 ; ORGANISM: Propionibacterium acnes
Db 61 GGGGQSGGGPGAEAAI 77 PCT-US02-32727-25717
; Sequence 25717, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglas, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 125717 LENGTH: 73
TYPE: PRT
ORGANISM: Propioni acnes
FEATURE:
NAME/KEY: unsure
LOCATION: (44)
OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-32727-25717
Query Match Score 47; DB 1; Length 73;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSQEOPRGGTTSSEQ 18
Db 45 LDGDGHRRAGGGDEERQ 62
RESULT 8 ;
; Sequence 25374, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglas, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 29374 LENGTH: 73
TYPE: PRT
; ORGANISM: Propionibacterium acnes
; Sequence 25717, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglas, John
TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 55403
; LENGTH: 220
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55403
Query Match Score 47; DB 5; Length 220;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GSGGQPRGGP 13 ;
Db 76 GRGASPRGGP 86
RESULT 11 ;
; Sequence 55403, Application US/09724676A
; GENERAL INFORMATION:

APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676A
 CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 9722
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 55403
 LENGTH: 220
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-724-676A-55403

Qy	3	GSGBQQPRGGGP	13	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	76	GROASPRGGGP	86	

RESULT 12
 PCT-US02-32727-10714

Qy	8	PRGGTSSSEQIM	20	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	26	PRASGPTSSSEPLV	38	

RESULT 13
 PCT-US02-32727-10714

Qy	3	GSGBQQPRGGGP	13	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	76	GROASPRGGGP	86	

RESULT 14
 US-10-276-774-1847

Qy	8	PRGGTSSSEQIM	20	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	26	PRASGPTSSSEPLV	38	

RESULT 14
 Sequence 10714, Application PC/US0232727

Qy	8	PRGGTSSSEQIM	20	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	26	PRASGPTSSSEPLV	38	

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer
 APPLICANT: Skeiky, Yasir
 APPLICANT: Persing, David
 APPLICANT: Bratia, Ajay
 APPLICANT: Maisonneuve, Jean Francois
 APPLICANT: Zhang, Yanni
 APPLICANT: Wang, Siping
 APPLICANT: Jen, Shyian
 APPLICANT: Lodes, Michael
 APPLICANT: Benson, Darin
 APPLICANT: Jones, Robert
 APPLICANT: Carter, Barrick
 APPLICANT: Barth, Brenda
 APPLICANT: Douglass, John

TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes v

FILE REFERENCE: 21021.554C1
 CURRENT APPLICATION NUMBER: PCT/US02/32727
 CURRENT FILING DATE: 2002-10-11
 NUMBER OF SEQ ID NOS: 30992
 SEQ ID NO 10714
 LENGTH: 94
 TYPE: PRT
 ORGANISM: Propioni acnes

Qy	8	PRGGTSSSEQIM	20	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	26	GROASPRGGGP	86	

RESULT 15
 US-09-724-676-64338

Qy	2	DGSESEQ-----PRGGTSSIE	17	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	64	EGAGPSPPPGIPRGGSSE	85	

RESULT 15
 US-09-724-676-64338

Qy	2	DGSESEQ-----PRGGTSSIE	17	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	64	EGAGPSPPPGIPRGGSSE	85	

GENERAL INFORMATION:

APPLICANT: Compugen LTD
 TITLE OF INVENTION: Variants of alternative splicing
 FILE REFERENCE: 129181.4 Compugen
 CURRENT APPLICATION NUMBER: US/09/724,676A
 CURRENT FILING DATE: 2000-11-28
 NUMBER OF SEQ ID NOS: 9722
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 64338
 LENGTH: 256
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-724-676-64338

Qy	1	MDSGEQQRGG--GPTSSIE	18	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	139	MDGGPGRFAFWEPTESSDE	158	

RESULT 13
 US-10-057-498-10714

Qy	8	PRGGTSSSEQIM	20	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	26	PRASGPTSSSEPLV	38	

RESULT 13
 US-10-057-498-10714

Qy	1	MDSGEQQRGG--GPTSSIE	18	Score 47; DB 5; Length 220; Best Local Similarity 72.7%; Pred. No. 42; Mismatches 8; Conservative 0; Indels 3; Gaps 0; Gaps 0;
Db	139	MDGGPGRFAFWEPTESSDE	158	

SEARCH COMPLETED: January 7, 2003, 12:36:59
 Job time : 11.7949 secs

Tue Jan 7 13:10:53 2003

us-09-876-204-3_1.rapn

